

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: BIRKELUND, Svend
CHRISTIANSEN, Gunna
HEBSGAARD PEDERSEN, Anna-Sofie
MYGIND, Per
KNUDSEN, Katrine
- (ii) TITLE OF INVENTION: SURFACE EXPOSED PROTEINS FROM CHLAMYDIA
PNEUMONIAE
- (iii) NUMBER OF SEQUENCES: 30
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
 - (B) STREET: 624 Ninth Street, N.W., Suite 300
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 20001
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/446,677
 - (B) FILING DATE: 24-MAR-2000
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/DK98/00266
 - (B) FILING DATE: 19-JUN-1998
- vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: DK 0744/97
 - (B) FILING DATE: 23-JUN-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: COOPER, Iver P.
 - (B) REGISTRATION NUMBER: 28,005
 - (C) REFERENCE/DOCKET NUMBER: BIRKELUND=1
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-628-5197
 - (B) TELEFAX: 202-737-3528

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 205...2987

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAATGTCGAA GAGAGCACTA ACCAGGAAAA TTGCGATTTC ATAAACCCAC TTTATTATTA 60
AATTCTTACT TGCATCATAT AAAATAGAAA ACTCAGAGAG TCAAGATAAA AATTCTTGAC 120
AGCTGTTTTG TCATCTTTAA CTTGATTAC TTATTTTGTT TCTATATTGA TGCGAATAGT 180
TCTCTAAAAA ACAAAGCAT TACC ATG AAG ACT TCG ATT CCT TGG GTT TTA 231
Met Lys Thr Ser Ile Pro Trp Val Leu
1 5

GTT TCC TCC GTG TTA GCT TTC TCA TGT CAC CTA CAG TCA CTA GCT AAC 279
Val Ser Ser Val Leu Ala Phe Ser Cys His Leu Gln Ser Leu Ala Asn
10 15 20 25

GAG GAA CTT TTA TCA CCT GAT GAT AGC TTT AAT GGA AAT ATC GAT TCA 327
Glu Glu Leu Leu Ser Pro Asp Asp Ser Phe Asn Gly Asn Ile Asp Ser
30 35 40

GGA ACG TTT ACT CCA AAA ACT TCA GCC ACA ACA TAT TCT CTA ACA GGA 375
Gly Thr Phe Thr Pro Lys Thr Ser Ala Thr Thr Tyr Ser Leu Thr Gly
45 50 55

GAT GTC TTC TTT TAC GAG CCT GGA AAA GGC ACT CCC TTA TCT GAC AGT 423
Asp Val Phe Phe Tyr Glu Pro Gly Lys Gly Thr Pro Leu Ser Asp Ser
60 65 70

TGT TTT AAG CAA ACC ACG GAC AAT CTT ACC TTC TTG GGG AAC GGT CAT 471
Cys Phe Lys Gln Thr Thr Asp Asn Leu Thr Phe Leu Gly Asn Gly His
75 80 85

AGC TTA ACG TTT GGC TTT ATA GAT GCT GGC ACT CAT GCA GGT GCT GCT 519
Ser Leu Thr Phe Gly Phe Ile Asp Ala Gly Thr His Ala Gly Ala Ala
90 95 100 105

GCA TCT ACA ACA GCA AAT AAG AAT CTT ACC TTC TCA GGG TTT TCC TTA 567
Ala Ser Thr Thr Ala Asn Lys Asn Leu Thr Phe Ser Gly Phe Ser Leu
110 115 120

CTG AGT TTT GAT TCC TCT CCT AGC ACA ACG GTT ACT ACA GGT CAG GGA 615
Leu Ser Phe Asp Ser Ser Pro Ser Thr Thr Val Thr Thr Gly Gln Gly
125 130 135

ACG CTT TCC TCA GCA GGA GGC GTA AAT TTA GAA AAT ATT CTT AAA CTT 663
Thr Leu Ser Ser Ala Gly Gly Val Asn Leu Glu Asn Ile Arg Lys Leu
140 145 150

GTA GTT GCT GGG AAT TTT TCT ACT GCA GAT GGT GGA GCT ATC AAA GGA 711
Val Val Ala Gly Asn Phe Ser Thr Ala Asp Gly Gly Ala Ile Lys Gly
155 160 165

GCG	TCT	TTC	CTT	TTA	ACT	GGC	ACT	TCT	GGA	GAT	GCT	CTT	TTT	AGT	AAC	759
Ala	Ser	Phe	Leu	Leu	Thr	Gly	Thr	Ser	Gly	Asp	Ala	Leu	Phe	Ser	Asn	
170					175				180						185	
AAC	TCT	TCA	TCA	ACA	AAG	GGA	GGA	GCA	ATT	GCT	ACT	ACA	GCA	GGC	GCT	807
Asn	Ser	Ser	Ser	Thr	Lys	Gly	Gly	Ala	Ile	Ala	Thr	Thr	Ala	Gly	Ala	
				190				195						200		
CGC	ATA	GCA	AAT	AAC	ACA	GGT	TAT	GTT	AGA	TTC	CTA	TCT	AAC	ATA	GCG	855
Arg	Ile	Ala	Asn	Asn	Thr	Gly	Tyr	Val	Arg	Phe	Leu	Ser	Asn	Ile	Ala	
			205					210					215			
TCT	ACG	TCA	GGA	GGC	GCT	ATC	GAT	GAT	GAA	GGC	ACG	TCG	ATA	CTA	TCG	903
Ser	Thr	Ser	Gly	Gly	Ala	Ile	Asp	Asp	Glu	Gly	Thr	Ser	Ile	Leu	Ser	
		220				225						230				
AAC	AAC	AAA	TTT	CTA	TAT	TTT	GAA	GGG	AAT	GCA	GCG	AAA	ACT	ACT	GGC	951
Asn	Asn	Lys	Phe	Leu	Tyr	Phe	Glu	Gly	Asn	Ala	Ala	Lys	Thr	Thr	Gly	
	235					240					245					
GGT	GCG	ATC	TGC	AAC	ACC	AAG	GCG	AGT	GGA	TCT	CCT	GAA	CTG	ATA	ATC	999
Gly	Ala	Ile	Cys	Asn	Thr	Lys	Ala	Ser	Gly	Ser	Pro	Glu	Leu	Ile	Ile	
250					255				260						265	
TCT	AAC	AAT	AAG	ACT	CTG	ATC	TTT	GCT	TCA	AAC	GTA	GCA	GAA	ACA	AGC	1047
Ser	Asn	Asn	Lys	Thr	Leu	Ile	Phe	Ala	Ser	Asn	Val	Ala	Glu	Thr	Ser	
				270				275						280		
GGT	GGC	GCC	ATC	CAT	GCT	AAA	AAG	CTA	GCC	CTT	TCC	TCT	GGA	GGC	TTT	1095
Gly	Gly	Ala	Ile	His	Ala	Lys	Lys	Leu	Ala	Leu	Ser	Ser	Gly	Gly	Phe	
			285					290					295			
ACA	GAG	TTT	CTA	CGA	AAT	AAT	GTC	TCA	TCA	GCA	ACT	CCT	AAG	GGG	GGT	1143
Thr	Glu	Phe	Leu	Arg	Asn	Asn	Val	Ser	Ser	Ala	Thr	Pro	Lys	Gly	Gly	
		300					305					310				
GCT	ATC	AGC	ATC	GAT	GCC	TCA	GGA	GAG	CTC	AGT	CTT	TCT	GCA	GAG	ACA	1191
Ala	Ile	Ser	Ile	Asp	Ala	Ser	Gly	Glu	Leu	Ser	Leu	Ser	Ala	Glu	Thr	
	315					320					325					
GGA	AAC	ATT	ACC	TTT	GTA	AGA	AAT	ACC	CTT	ACA	ACA	ACC	GGA	AGT	ACC	1239
Gly	Asn	Ile	Thr	Phe	Val	Arg	Asn	Thr	Leu	Thr	Thr	Thr	Gly	Ser	Thr	
330					335				340						345	
GAT	ACT	CCT	AAA	CGT	AAT	GCG	ATC	AAC	ATA	GGA	AGT	AAC	GGG	AAA	TTC	1287
Asp	Thr	Pro	Lys	Arg	Asn	Ala	Ile	Asn	Ile	Gly	Ser	Asn	Gly	Lys	Phe	
				350				355						360		
ACG	GAA	TTA	CGG	GCT	GCT	AAA	AAT	CAT	ACA	ATT	TTC	TTC	TAT	GAT	CCC	1335
Thr	Glu	Leu	Arg	Ala	Ala	Lys	Asn	His	Thr	Ile	Phe	Phe	Tyr	Asp	Pro	
			365					370					375			
ATC	ACT	TCA	GAA	GGA	ACC	TCA	TCA	GAC	GTA	TTG	AAG	ATA	AAT	AAC	GGC	1383
Ile	Thr	Ser	Glu	Gly	Thr	Ser	Ser	Asp	Val	Leu	Lys	Ile	Asn	Asn	Gly	
		380					385					390				

TCT	GCG	GGA	GCT	CTC	AAT	CCA	TAT	CAA	GGA	ACG	ATT	CTA	TTT	TCT	GGA	1431
Ser	Ala	Gly	Ala	Leu	Asn	Pro	Tyr	Gln	Gly	Thr	Ile	Leu	Phe	Ser	Gly	
	395					400					405					
GAA	ACC	CTA	ACA	GCA	GAT	GAA	CTT	AAA	GTT	GCT	GAC	AAT	TTA	AAA	TCT	1479
Glu	Thr	Leu	Thr	Ala	Asp	Glu	Leu	Lys	Val	Ala	Asp	Asn	Leu	Lys	Ser	
410					415				420						425	
TCA	TTC	ACG	CAG	CCA	GTC	TCC	CTA	TCC	GGA	GGA	AAG	TTA	TTG	CTA	CAA	1527
Ser	Phe	Thr	Gln	Pro	Val	Ser	Leu	Ser	Gly	Gly	Lys	Leu	Leu	Leu	Gln	
				430					435						440	
AAG	GGA	GTC	ACT	TTA	GAG	AGC	ACG	AGC	TTC	TCT	CAA	GAG	GCC	GGT	TCT	1575
Lys	Gly	Val	Thr	Leu	Glu	Ser	Thr	Ser	Phe	Ser	Gln	Glu	Ala	Gly	Ser	
			445					450					455			
CTC	CTC	GGC	ATG	GAT	TCA	GGA	ACG	ACA	TTA	TCA	ACT	ACA	GCT	GGG	AGT	1623
Leu	Leu	Gly	Met	Asp	Ser	Gly	Thr	Thr	Leu	Ser	Thr	Thr	Ala	Gly	Ser	
		460					465						470			
ATT	ACA	ATC	ACG	AAC	CTA	GGA	ATC	AAT	GTT	GAC	TCC	TTA	GGT	CTT	AAG	1671
Ile	Thr	Ile	Thr	Asn	Leu	Gly	Ile	Asn	Val	Asp	Ser	Leu	Gly	Leu	Lys	
	475					480					485					
CAG	CCC	GTC	AGC	CTA	ACA	GCA	AAA	GGT	GCT	TCA	AAT	AAA	GTG	ATC	GTA	1719
Gln	Pro	Val	Ser	Leu	Thr	Ala	Lys	Gly	Ala	Ser	Asn	Lys	Val	Ile	Val	
490						495				500					505	
TCT	GGG	AAG	CTC	AAC	CTG	ATT	GAT	ATT	GAA	GGG	AAC	ATT	TAT	GAA	AGT	1767
Ser	Gly	Lys	Leu	Asn	Leu	Ile	Asp	Ile	Glu	Gly	Asn	Ile	Tyr	Glu	Ser	
				510					515					520		
CAT	ATG	TTC	AGC	CAT	GAC	CAG	CTC	TTC	TCT	CTA	TTA	AAA	ATC	ACG	GTT	1815
His	Met	Phe	Ser	His	Asp	Gln	Leu	Phe	Ser	Leu	Leu	Lys	Ile	Thr	Val	
			525					530					535			
GAT	GCT	GAT	GTT	GAT	ACT	AAC	GTT	GAC	ATC	AGC	AGC	CTT	ATC	CCT	GTT	1863
Asp	Ala	Asp	Val	Asp	Thr	Asn	Val	Asp	Ile	Ser	Ser	Leu	Ile	Pro	Val	
		540					545					550				
CCT	GCT	GAG	GAT	CCT	AAT	TCA	GAA	TAC	GGA	TTC	CAA	GGA	CAA	TGG	AAT	1911
Pro	Ala	Glu	Asp	Pro	Asn	Ser	Glu	Tyr	Gly	Phe	Gln	Gly	Gln	Trp	Asn	
	555					560					565					
GTT	AAT	TGG	ACT	ACG	GAT	ACA	GCT	ACA	AAT	ACA	AAA	GAG	GCC	ACG	GCA	1959
Val	Asn	Trp	Thr	Thr	Asp	Thr	Ala	Thr	Asn	Thr	Lys	Glu	Ala	Thr	Ala	
570					575				580						585	
ACT	TGG	ACC	AAA	ACA	GGA	TTT	GTT	CCC	AGC	CCC	GAA	AGA	AAA	TCT	GCG	2007
Thr	Trp	Thr	Lys	Thr	Gly	Phe	Val	Pro	Ser	Pro	Glu	Arg	Lys	Ser	Ala	
				590					595					600		
TTA	GTA	TGC	AAT	ACC	CTA	TGG	GGA	GTC	TTT	ACT	GAC	ATT	CGC	TCT	CTG	2055
Leu	Val	Cys	Asn	Thr	Leu	Trp	Gly	Val	Phe	Thr	Asp	Ile	Arg	Ser	Leu	
			605					610					615			

CAA	CAG	CTT	GTA	GAG	ATC	GGC	GCA	ACT	GGT	ATG	GAA	CAC	AAA	CAA	GGT	2103
Gln	Gln	Leu	Val	Glu	Ile	Gly	Ala	Thr	Gly	Met	Glu	His	Lys	Gln	Gly	
		620					625						630			
TTC	TGG	GTT	TCC	TCC	ATG	ACG	AAC	TTC	CTG	CAT	AAG	ACT	GGA	GAT	GAA	2151
Phe	Trp	Val	Ser	Ser	Met	Thr	Asn	Phe	Leu	His	Lys	Thr	Gly	Asp	Glu	
	635					640					645					
AAT	CGC	AAA	GGC	TTC	CGT	CAT	ACC	TCT	GGA	GGC	TAC	GTC	ATC	GGT	GGA	2199
Asn	Arg	Lys	Gly	Phe	Arg	His	Thr	Ser	Gly	Gly	Tyr	Val	Ile	Gly	Gly	
650					655					660					665	
AGT	GCT	CAC	ACT	CCT	AAA	GAC	GAC	CTA	TTT	ACC	TTT	GCG	TTC	TGC	CAT	2247
Ser	Ala	His	Thr	Pro	Lys	Asp	Asp	Leu	Phe	Thr	Phe	Ala	Phe	Cys	His	
				670					675					680		
CTC	TTT	GCT	AGA	GAC	AAA	GAT	TGT	TTT	ATC	GCT	CAC	AAC	AAC	TCT	AGA	2295
Leu	Phe	Ala	Arg	Asp	Lys	Asp	Cys	Phe	Ile	Ala	His	Asn	Asn	Ser	Arg	
			685					690						695		
ACC	TAC	GGT	GGA	ACT	TTA	TTC	TTC	AAG	CAC	TCT	CAT	ACC	CTA	CAA	CCC	2343
Thr	Tyr	Gly	Gly	Thr	Leu	Phe	Phe	Lys	His	Ser	His	Thr	Leu	Gln	Pro	
		700				705						710				
CAA	AAC	TAT	TTG	AGA	TTA	GGA	AGA	GCA	AAG	TTT	TCT	GAA	TCA	GCT	ATA	2391
Gln	Asn	Tyr	Leu	Arg	Leu	Gly	Arg	Ala	Lys	Phe	Ser	Glu	Ser	Ala	Ile	
	715					720					725					
GAA	AAA	TTC	CCT	AGG	GAA	ATT	CCC	CTA	GCC	TTG	GAT	GTC	CAA	GTT	TCG	2439
Glu	Lys	Phe	Pro	Arg	Glu	Ile	Pro	Leu	Ala	Leu	Asp	Val	Gln	Val	Ser	
730					735					740					745	
TTC	AGC	CAT	TCA	GAC	AAC	CGT	ATG	GAA	ACG	CAC	TAT	ACC	TCA	TTG	CCA	2487
Phe	Ser	His	Ser	Asp	Asn	Arg	Met	Glu	Thr	His	Tyr	Thr	Ser	Leu	Pro	
				750					755					760		
GAA	TCC	GAA	GGT	TCT	TGG	AGC	AAC	GAG	TGT	ATA	GCT	GGT	GGT	ATC	GGC	2535
Glu	Ser	Glu	Gly	Ser	Trp	Ser	Asn	Glu	Cys	Ile	Ala	Gly	Gly	Ile	Gly	
			765					770					775			
CTA	GAC	CTT	CCT	TTT	GTT	CTT	TCC	AAC	CCA	CAT	CCT	CTT	TTC	AAG	ACC	2583
Leu	Asp	Leu	Pro	Phe	Val	Leu	Ser	Asn	Pro	His	Pro	Leu	Phe	Lys	Thr	
			780					785					790			
TTC	ATT	CCA	CAG	ATG	AAA	GTC	GAA	ATG	GTT	TAT	GTA	TCA	CAA	AAT	AGC	2631
Phe	Ile	Pro	Gln	Met	Lys	Val	Glu	Met	Val	Tyr	Val	Ser	Gln	Asn	Ser	
	795					800					805					
TTC	TTC	GAA	AGC	TCT	AGT	GAT	GGC	CGT	GGT	TTT	AGT	ATT	GGA	AGG	CTG	2679
Phe	Phe	Glu	Ser	Ser	Ser	Asp	Gly	Arg	Gly	Phe	Ser	Ile	Gly	Arg	Leu	
810					815					820					825	
CTT	AAC	CTC	TCG	ATT	CCT	GTG	GGT	GCG	AAA	TTC	GTG	CAG	GGG	GAT	ATC	2727
Leu	Asn	Leu	Ser	Ile	Pro	Val	Gly	Ala	Lys	Phe	Val	Gln	Gly	Asp	Ile	
				830					835					840		

GGA GAT TCC TAC ACC TAT GAT CTC TCA GGA TTC TTT GTT TCC GAT GTC 2775
 Gly Asp Ser Tyr Thr Tyr Asp Leu Ser Gly Phe Phe Val Ser Asp Val
 845 850 855
 TAT CGT AAC AAT CCC CAA TCT ACA GCG ACT CTT GTG ATG AGC CCA GAC 2823
 Tyr Arg Asn Asn Pro Gln Ser Thr Ala Thr Leu Val Met Ser Pro Asp
 860 865 870
 TCT TGG AAA ATT CGC GGT GGC AAT CTT TCA AGA CAG GCA TTT TTA CTG 2871
 Ser Trp Lys Ile Arg Gly Gly Asn Leu Ser Arg Gln Ala Phe Leu Leu
 875 880 885
 AGG GGT AGC AAC AAC TAC GTC TAC AAC TCC AAT TGT GAG CTC TTC GGA 2919
 Arg Gly Ser Asn Asn Tyr Val Tyr Asn Ser Asn Cys Glu Leu Phe Gly
 890 895 900 905
 CAT TAC GCT ATG GAA CTC CGT GGA TCT TCA AGG AAC TAC AAT GTA GAT 2967
 His Tyr Ala Met Glu Leu Arg Gly Ser Ser Arg Asn Tyr Asn Val Asp
 910 915 920
 GTT GGT ACC AAA CTC CGA TT CTAGATTGCT AAAACTCCCT AGTTCTTCTA GGGAG 3022
 Val Gly Thr Lys Leu Arg Phe
 925
 TTTTCTCATA CTTTtaggga AATATTTGCT ATAGGGAATG CTTTCCTTGC AAACGTGAAA 3082
 AAATAACATT TGTCCCTCTT CAAAAAAGAT TTCTTTTAAT AATTTCTAGT TATAATTTTA 3142
 TTTTAAAAAC AGTTAAATAA TTAATAGACA ATAATCTATT CTTATTGACT TCTTTTTT 3200

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Thr Ser Ile Pro Trp Val Leu Val Ser Ser Val Leu Ala Phe
 1 5 10 15
 Ser Cys His Leu Gln Ser Leu Ala Asn Glu Glu Leu Leu Ser Pro Asp
 20 25 30
 Asp Ser Phe Asn Gly Asn Ile Asp Ser Gly Thr Phe Thr Pro Lys Thr
 35 40 45
 Ser Ala Thr Thr Tyr Ser Leu Thr Gly Asp Val Phe Phe Tyr Glu Pro
 50 55 60
 Gly Lys Gly Thr Pro Leu Ser Asp Ser Cys Phe Lys Gln Thr Thr Asp
 65 70 75 80

Asn	Leu	Thr	Phe	Leu	Gly	Asn	Gly	His	Ser	Leu	Thr	Phe	Gly	Phe	Ile		
				85					90					95			
Asp	Ala	Gly	Thr	His	Ala	Gly	Ala	Ala	Ala	Ser	Thr	Thr	Ala	Asn	Lys		
			100				105						110				
Asn	Leu	Thr	Phe	Ser	Gly	Phe	Ser	Leu	Leu	Ser	Phe	Asp	Ser	Ser	Pro		
		115					120					125					
Ser	Thr	Thr	Val	Thr	Thr	Gly	Gln	Gly	Thr	Leu	Ser	Ser	Ala	Gly	Gly		
	130					135					140						
Val	Asn	Leu	Glu	Asn	Ile	Arg	Lys	Leu	Val	Val	Ala	Gly	Asn	Phe	Ser		
145					150					155					160		
Thr	Ala	Asp	Gly	Gly	Ala	Ile	Lys	Gly	Ala	Ser	Phe	Leu	Leu	Thr	Gly		
			165					170						175			
Thr	Ser	Gly	Asp	Ala	Leu	Phe	Ser	Asn	Asn	Ser	Ser	Ser	Thr	Lys	Gly		
		180						185					190				
Gly	Ala	Ile	Ala	Thr	Thr	Ala	Gly	Ala	Arg	Ile	Ala	Asn	Asn	Thr	Gly		
	195						200					205					
Tyr	Val	Arg	Phe	Leu	Ser	Asn	Ile	Ala	Ser	Thr	Ser	Gly	Gly	Ala	Ile		
	210					215					220						
Asp	Asp	Glu	Gly	Thr	Ser	Ile	Leu	Ser	Asn	Asn	Lys	Phe	Leu	Tyr	Phe		
225					230					235					240		
Glu	Gly	Asn	Ala	Ala	Lys	Thr	Thr	Gly	Gly	Ala	Ile	Cys	Asn	Thr	Lys		
			245					250						255			
Ala	Ser	Gly	Ser	Pro	Glu	Leu	Ile	Ile	Ser	Asn	Asn	Lys	Thr	Leu	Ile		
		260						265					270				
Phe	Ala	Ser	Asn	Val	Ala	Glu	Thr	Ser	Gly	Gly	Ala	Ile	His	Ala	Lys		
	275						280					285					
Lys	Leu	Ala	Leu	Ser	Ser	Gly	Gly	Phe	Thr	Glu	Phe	Leu	Arg	Asn	Asn		
	290					295					300						
Val	Ser	Ser	Ala	Thr	Pro	Lys	Gly	Gly	Ala	Ile	Ser	Ile	Asp	Ala	Ser		
305					310					315					320		
Gly	Glu	Leu	Ser	Leu	Ser	Ala	Glu	Thr	Gly	Asn	Ile	Thr	Phe	Val	Arg		
			325						330					335			
Asn	Thr	Leu	Thr	Thr	Thr	Gly	Ser	Thr	Asp	Thr	Pro	Lys	Arg	Asn	Ala		
		340						345					350				
Ile	Asn	Ile	Gly	Ser	Asn	Gly	Lys	Phe	Thr	Glu	Leu	Arg	Ala	Ala	Lys		
	355					360						365					
Asn	His	Thr	Ile	Phe	Phe	Tyr	Asp	Pro	Ile	Thr	Ser	Glu	Gly	Thr	Ser		
	370					375					380						
Ser	Asp	Val	Leu	Lys	Ile	Asn	Asn	Gly	Ser	Ala	Gly	Ala	Leu	Asn	Pro		
385					390					395					400		

Tyr Gln Gly Thr Ile Leu Phe Ser Gly Glu Thr Leu Thr Ala Asp Glu
 405 410 415
 Leu Lys Val Ala Asp Asn Leu Lys Ser Ser Phe Thr Gln Pro Val Ser
 420 425 430
 Leu Ser Gly Gly Lys Leu Leu Leu Gln Lys Gly Val Thr Leu Glu Ser
 435 440 445
 Thr Ser Phe Ser Gln Glu Ala Gly Ser Leu Leu Gly Met Asp Ser Gly
 450 455 460
 Thr Thr Leu Ser Thr Thr Ala Gly Ser Ile Thr Ile Thr Asn Leu Gly
 465 470 475 480
 Ile Asn Val Asp Ser Leu Gly Leu Lys Gln Pro Val Ser Leu Thr Ala
 485 490 495
 Lys Gly Ala Ser Asn Lys Val Ile Val Ser Gly Lys Leu Asn Leu Ile
 500 505 510
 Asp Ile Glu Gly Asn Ile Tyr Glu Ser His Met Phe Ser His Asp Gln
 515 520 525
 Leu Phe Ser Leu Leu Lys Ile Thr Val Asp Ala Asp Val Asp Thr Asn
 530 535 540
 Val Asp Ile Ser Ser Leu Ile Pro Val Pro Ala Glu Asp Pro Asn Ser
 545 550 555 560
 Glu Tyr Gly Phe Gln Gly Gln Trp Asn Val Asn Trp Thr Thr Asp Thr
 565 570 575
 Ala Thr Asn Thr Lys Glu Ala Thr Ala Thr Trp Thr Lys Thr Gly Phe
 580 585 590
 Val Pro Ser Pro Glu Arg Lys Ser Ala Leu Val Cys Asn Thr Leu Trp
 595 600 605
 Gly Val Phe Thr Asp Ile Arg Ser Leu Gln Gln Leu Val Glu Ile Gly
 610 615 620
 Ala Thr Gly Met Glu His Lys Gln Gly Phe Trp Val Ser Ser Met Thr
 625 630 635 640
 Asn Phe Leu His Lys Thr Gly Asp Glu Asn Arg Lys Gly Phe Arg His
 645 650 655
 Thr Ser Gly Gly Tyr Val Ile Gly Gly Ser Ala His Thr Pro Lys Asp
 660 665 670
 Asp Leu Phe Thr Phe Ala Phe Cys His Leu Phe Ala Arg Asp Lys Asp
 675 680 685
 Cys Phe Ile Ala His Asn Asn Ser Arg Thr Tyr Gly Gly Thr Leu Phe
 690 695 700

Phe	Lys	His	Ser	His	Thr	Leu	Gln	Pro	Gln	Asn	Tyr	Leu	Arg	Leu	Gly	705	710	715	720
Arg	Ala	Lys	Phe	Ser	Glu	Ser	Ala	Ile	Glu	Lys	Phe	Pro	Arg	Glu	Ile	725	730	735	
Pro	Leu	Ala	Leu	Asp	Val	Gln	Val	Ser	Phe	Ser	His	Ser	Asp	Asn	Arg	740	745	750	
Met	Glu	Thr	His	Tyr	Thr	Ser	Leu	Pro	Glu	Ser	Glu	Gly	Ser	Trp	Ser	755	760	765	
Asn	Glu	Cys	Ile	Ala	Gly	Gly	Ile	Gly	Leu	Asp	Leu	Pro	Phe	Val	Leu	770	775	780	
Ser	Asn	Pro	His	Pro	Leu	Phe	Lys	Thr	Phe	Ile	Pro	Gln	Met	Lys	Val	785	790	795	800
Glu	Met	Val	Tyr	Val	Ser	Gln	Asn	Ser	Phe	Phe	Glu	Ser	Ser	Ser	Asp	805	810	815	
Gly	Arg	Gly	Phe	Ser	Ile	Gly	Arg	Leu	Leu	Asn	Leu	Ser	Ile	Pro	Val	820	825	830	
Gly	Ala	Lys	Phe	Val	Gln	Gly	Asp	Ile	Gly	Asp	Ser	Tyr	Thr	Tyr	Asp	835	840	845	
Leu	Ser	Gly	Phe	Phe	Val	Ser	Asp	Val	Tyr	Arg	Asn	Asn	Pro	Gln	Ser	850	855	860	
Thr	Ala	Thr	Leu	Val	Met	Ser	Pro	Asp	Ser	Trp	Lys	Ile	Arg	Gly	Gly	865	870	875	880
Asn	Leu	Ser	Arg	Gln	Ala	Phe	Leu	Leu	Arg	Gly	Ser	Asn	Asn	Tyr	Val	885	890	895	
Tyr	Asn	Ser	Asn	Cys	Glu	Leu	Phe	Gly	His	Tyr	Ala	Met	Glu	Leu	Arg	900	905	910	
Gly	Ser	Ser	Arg	Asn	Tyr	Asn	Val	Asp	Val	Gly	Thr	Lys	Leu	Arg	Phe	915	920	925	

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGAAATCGC	AATTTTCCTG	GTTAGTGCTC	TCTTCGACAT	TGGCATGTTT	TACTAGTTGT	60
TCCACTGTTT	TTGCTGCAAC	TGCTGAAAAT	ATAGGCCCTT	CTGATAGCTT	TGACGGAAGT	120
ACTAACACAG	GCACCTATAC	TCCTAAAAAT	ACGACTACTG	GAATAGACTA	TACTCTGACA	180
GGAGATATAA	CTCTGCAAAA	CCTTGGGGAT	TCGGCAGCTT	TAACGAAGGG	TTGTTTTTCT	240

GACACTACGG	AATCTTTAAG	CTTTGCCGGT	AAGGGGTA	CACTTTCTTT	TTTAAATATT	300
AAGTCTAGTG	CTGAAGGCGC	AGCACTTTCT	GTTACAAC	ATAAAAAATCT	GTCGCTAACA	360
GGATTTTCGA	GTCTTACTTT	CTTAGCGGCC	CCATCATCGG	TAATCACAAC	CCCCTCAGGA	420
AAAGGTGCAG	TTAAATGTGG	AGGGGATCTT	ACATTTGATA	ACAATGGAAC	TATTTTATTT	480
AAACAAGATT	ACTGTGAGGA	AAATGGCGGA	GCCATTTCTA	CCAAGAATCT	TTCTTTGAAA	540
AACAGCACGG	GATCGATTTT	TTTTGAAGGG	AATAAATCGA	GCGCAACAGG	GAAAAAAGGT	600
GGGGCTATTT	GTGCTACTGG	TACTGTAGAT	ATTACAAATA	ATACGGCTCC	TACCCTCTTC	660
TCGAACAATA	TTGCTGAAGC	TGCAGGTGGA	GCTATAAATA	GCACAGGAAA	CTGTACAATT	720
ACAGGGAATA	CGTCTCTTGT	ATTTTCTGAA	AATAGTGTGA	CAGCGACCGC	AGGAAATGGA	780
GGAGCTCTTT	CTGGAGATGC	CGATGTTACC	ATATCTGGGA	ATCAGAGTGT	AACCTTCTCA	840
GGAACCAAG	CTGTAGCTAA	TGGCGGAGCC	ATTTATGCTA	AGAAGCTTAC	ACTGGCTTCC	900
GGGGGGGGGG	GGGGTATCTC	CTTTTCTAAC	AATATAGTCC	AAGGTACCAC	TGCAGGTAAT	960
GGTGGAGCCA	TTTCTATACT	GGCAGCTGGA	GAGTGTAGTC	TTTCAGCAGA	AGCAGGGGAC	1020
ATTACCTTCA	ATGGGAATGC	CATTGTTGCA	ACTACACCAC	AAACTACAAA	AAGAAATTCT	1080
ATTGACATAG	GATCTACTGC	AAAGATCACG	AATTTACGTG	CAATATCTGG	GCATAGCATC	1140
TTTTTCTACG	ATCCGATTAC	TGCTAATACG	GCTGCGGATT	CTACAGATAC	TTTAAATCTC	1200
AATAAGGCTG	ATGCAGGTAA	TAGTACAGAT	TATAGTGGGT	CGATTGTTTT	TTCTGGTGAA	1260
AAGCTCTCTG	AAGATGAAGC	AAAAGTTGCA	GACAACCTCA	CTTCTACGCT	GAAGCAGCCT	1320
GTAACCTCTAA	CTGCAGGAAA	TTTAGTACTT	AAACGTGGTG	TCACTCTCGA	TACGAAAGGC	1380
TTTACTCAGA	CCGCGGGTTC	CTCTGTTATT	ATGGATGCGG	GCACAACGTT	AAAAGCAAGT	1440
ACAGAGGAGG	TCACCTTAAC	AGGTCTTTCC	ATTCTGTAG	ACTCTTTAGG	CGAGGGTAAG	1500
AAAGTTGTAA	TTGCTGCTTC	TGCAGCAAGT	AAAAATGTAG	CCCTTAGTGG	TCCGATTCTT	1560
CTTTTGGATA	ACCAAGGGAA	TGCTTATGAA	AATCACGACT	TAGGAAAAAC	TCAAGACTTT	1620
TCATTTGTGC	AGCTCTCTGC	TCTGGGTACT	GCAACAAC	CAGATGTTCC	AGCGGTTCC	1680
ACAGTAGCAA	CTCCTACGCA	CTATGGGTAT	CAAGGTACTT	GGGGAATGAC	TTGGGTTGAT	1740
GATACCGCAA	GCACCTCAA	GACTAAGACA	CGCAGATTAG	CTTGGACCAA	TACAGGCTAC	1800
CTTCCGAATC	CTGAGCGTCA	AGGACCTTTA	GTTCTTAATA	GCCTTTGGGG	ATCTTTTTC	1860
GACATCCAAG	CGATTCAAGG	TGTCATAGAG	AGAAGTGCTT	TGACTCTTTG	TTCAGATCGA	1920
GGCTTCTGGG	CTGCGGGAGT	CGCCAATTTT	TTAGATAAAG	ATAAGAAAGG	GGAAAAACGC	1980
AAATACCGTC	ATAAATCTGG	TGGATATGCT	ATCGGAGGTG	CAGCGCAAAC	TTGTTCTGAA	2040
AACTTAATTA	GCTTTGCCTT	TTGCCAACTC	TTTGGTAGCG	ATAAAGATTT	CTTAGTCGCT	2100
AAAAATCATA	CTGATACCTA	TGCAGGAGCC	TTCTATATCC	AACACATTAC	AGAATGTAGT	2160
GGGTTTCATG	GTTGTCTCTT	AGATAAACTT	CCTGGCTCTT	GGAGTCATAA	ACCCCTCGTT	2220
TTAGAAGGGC	AGCTCGCTTA	TAGCCACGTC	AGTAATGATC	TGAAGACAAA	GTATACTGCG	2280
TATCCTGAGG	TGAAAGGTTT	TTGGGGGAAT	AATGCTTTTA	ACATGATGTT	GGGAGCTTCT	2340
TCTCATTCTT	ATCCTGAATA	CCTGCATTGT	TTTGATACCT	ATGCTCCATA	CATCAAAC	2400
AATCTGACCT	ATATACGTCA	GGACAGCTTC	TCGGAGAAAG	GTACAGAAGG	AAGATCTTTT	2460
GATGACAGCA	ACCTCTTCAA	TTTATCTTTG	CCTATAGGGG	TGAAGTTTGA	GAAGTTCTCT	2520
GATTGTAATG	ACTTTTCTTA	TGATCTGACT	TTATCCTATG	TTCTGATCT	TATCCGCAAT	2580
GATCCCAAAT	GCACTACAGC	ACTTGTAATC	AGCGGAGCCT	CTTGGGAAAC	TTATGCCAAT	2640
AACTTAGCAC	GACAGGCCTT	GCAAGTGCGT	GCAGGCAGTC	ACTACGCCTT	CTCTCCTATG	2700
TTTGAAGTGC	TCGGCCAGTT	TGTCTTTGAA	GTTCTGTGGT	CCTCACGGAT	TTATAATGTA	2760
GATCTTGGGG	GTAAGTTCCA	ATTCTAGGAG	CGTCTCTCAT	GTCTCAGAAA	TTCTG	2815

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Lys Ser Gln Phe Ser Trp Leu Val Leu Ser Ser Thr Leu Ala Cys
 1 5 10 15

Phe Thr Ser Cys Ser Thr Val Phe Ala Ala Thr Ala Glu Asn Ile Gly
 20 25 30
 Pro Ser Asp Ser Phe Asp Gly Ser Thr Asn Thr Gly Thr Tyr Thr Pro
 35 40 45
 Lys Asn Thr Thr Thr Gly Ile Asp Tyr Thr Leu Thr Gly Asp Ile Thr
 50 55 60
 Leu Gln Asn Leu Gly Asp Ser Ala Ala Leu Thr Lys Gly Cys Phe Ser
 65 70 75 80
 Asp Thr Thr Glu Ser Leu Ser Phe Ala Gly Lys Gly Tyr Ser Leu Ser
 85 90 95
 Phe Leu Asn Ile Lys Ser Ser Ala Glu Gly Ala Ala Leu Ser Val Thr
 100 105 110
 Thr Asp Lys Asn Leu Ser Leu Thr Gly Phe Ser Ser Leu Thr Phe Leu
 115 120 125
 Ala Ala Pro Ser Ser Val Ile Thr Thr Pro Ser Gly Lys Gly Ala Val
 130 135 140
 Lys Cys Gly Gly Asp Leu Thr Phe Asp Asn Asn Gly Thr Ile Leu Phe
 145 150 155 160
 Lys Gln Asp Tyr Cys Glu Glu Asn Gly Gly Ala Ile Ser Thr Lys Asn
 165 170 175
 Leu Ser Leu Lys Asn Ser Thr Gly Ser Ile Ser Phe Glu Gly Asn Lys
 180 185 190
 Ser Ser Ala Thr Gly Lys Lys Gly Gly Ala Ile Cys Ala Thr Gly Thr
 195 200 205
 Val Asp Ile Thr Asn Asn Thr Ala Pro Thr Leu Phe Ser Asn Asn Ile
 210 215 220
 Ala Glu Ala Ala Gly Gly Ala Ile Asn Ser Thr Gly Asn Cys Thr Ile
 225 230 235 240
 Thr Gly Asn Thr Ser Leu Val Phe Ser Glu Asn Ser Val Thr Ala Thr
 245 250 255
 Ala Gly Asn Gly Gly Ala Leu Ser Gly Asp Ala Asp Val Thr Ile Ser
 260 265 270
 Gly Asn Gln Ser Val Thr Phe Ser Gly Asn Gln Ala Val Ala Asn Gly
 275 280 285
 Gly Ala Ile Tyr Ala Lys Lys Leu Thr Leu Ala Ser Gly Gly Gly Gly
 290 295 300
 Gly Ile Ser Phe Ser Asn Asn Ile Val Gln Gly Thr Thr Ala Gly Asn
 305 310 315 320

Gly Gly Ala Ile Ser Ile Leu Ala Ala Gly Glu Cys Ser Leu Ser Ala
 325 330 335
 Glu Ala Gly Asp Ile Thr Phe Asn Gly Asn Ala Ile Val Ala Thr Thr
 340 345 350
 Pro Gln Thr Thr Lys Arg Asn Ser Ile Asp Ile Gly Ser Thr Ala Lys
 355 360 365
 Ile Thr Asn Leu Arg Ala Ile Ser Gly His Ser Ile Phe Phe Tyr Asp
 370 375 380
 Pro Ile Thr Ala Asn Thr Ala Ala Asp Ser Thr Asp Thr Leu Asn Leu
 385 390 395 400
 Asn Lys Ala Asp Ala Gly Asn Ser Thr Asp Tyr Ser Gly Ser Ile Val
 405 410 415
 Phe Ser Gly Glu Lys Leu Ser Glu Asp Glu Ala Lys Val Ala Asp Asn
 420 425 430
 Leu Thr Ser Thr Leu Lys Gln Pro Val Thr Leu Thr Ala Gly Asn Leu
 435 440 445
 Val Leu Lys Arg Gly Val Thr Leu Asp Thr Lys Gly Phe Thr Gln Thr
 450 455 460
 Ala Gly Ser Ser Val Ile Met Asp Ala Gly Thr Thr Leu Lys Ala Ser
 465 470 475 480
 Thr Glu Glu Val Thr Leu Thr Gly Leu Ser Ile Pro Val Asp Ser Leu
 485 490 495
 Gly Glu Gly Lys Lys Val Val Ile Ala Ala Ser Ala Ala Ser Lys Asn
 500 505 510
 Val Ala Leu Ser Gly Pro Ile Leu Leu Leu Asp Asn Gln Gly Asn Ala
 515 520 525
 Tyr Glu Asn His Asp Leu Gly Lys Thr Gln Asp Phe Ser Phe Val Gln
 530 535 540
 Leu Ser Ala Leu Gly Thr Ala Thr Thr Thr Asp Val Pro Ala Val Pro
 545 550 555 560
 Thr Val Ala Thr Pro Thr His Tyr Gly Tyr Gln Gly Thr Trp Gly Met
 565 570 575
 Thr Trp Val Asp Asp Thr Ala Ser Thr Pro Lys Thr Lys Thr Ala Thr
 580 585 590
 Leu Ala Trp Thr Asn Thr Gly Tyr Leu Pro Asn Pro Glu Arg Gln Gly
 595 600 605
 Pro Leu Val Pro Asn Ser Leu Trp Gly Ser Phe Ser Asp Ile Gln Ala
 610 615 620

Ile	Gln	Gly	Val	Ile	Glu	Arg	Ser	Ala	Leu	Thr	Leu	Cys	Ser	Asp	Arg	625	630	635	640
Gly	Phe	Trp	Ala	Ala	Gly	Val	Ala	Asn	Phe	Leu	Asp	Lys	Asp	Lys	Lys	645	650	655	
Gly	Glu	Lys	Arg	Lys	Tyr	Arg	His	Lys	Ser	Gly	Gly	Tyr	Ala	Ile	Gly	660	665	670	
Gly	Ala	Ala	Gln	Thr	Cys	Ser	Glu	Asn	Leu	Ile	Ser	Phe	Ala	Phe	Cys	675	680	685	
Gln	Leu	Phe	Gly	Ser	Asp	Lys	Asp	Phe	Leu	Val	Ala	Lys	Asn	His	Thr	690	695	700	
Asp	Thr	Tyr	Ala	Gly	Ala	Phe	Tyr	Ile	Gln	His	Ile	Thr	Glu	Cys	Ser	705	710	715	720
Gly	Phe	Ile	Gly	Cys	Leu	Leu	Asp	Lys	Leu	Pro	Gly	Ser	Trp	Ser	His	725	730	735	
Lys	Pro	Leu	Val	Leu	Glu	Gly	Gln	Leu	Ala	Tyr	Ser	His	Val	Ser	Asn	740	745	750	
Asp	Leu	Lys	Thr	Lys	Tyr	Thr	Ala	Tyr	Pro	Glu	Val	Lys	Gly	Ser	Trp	755	760	765	
Gly	Asn	Asn	Ala	Phe	Asn	Met	Met	Leu	Gly	Ala	Ser	Ser	His	Ser	Tyr	770	775	780	
Pro	Glu	Tyr	Leu	His	Cys	Phe	Asp	Thr	Tyr	Ala	Pro	Tyr	Ile	Lys	Leu	785	790	795	800
Asn	Leu	Thr	Tyr	Ile	Arg	Gln	Asp	Ser	Phe	Ser	Glu	Lys	Gly	Thr	Glu	805	810	815	
Gly	Arg	Ser	Phe	Asp	Asp	Ser	Asn	Leu	Phe	Asn	Leu	Ser	Leu	Pro	Ile	820	825	830	
Gly	Val	Lys	Phe	Glu	Lys	Phe	Ser	Asp	Cys	Asn	Asp	Phe	Ser	Tyr	Asp	835	840	845	
Leu	Thr	Leu	Ser	Tyr	Val	Pro	Asp	Leu	Ile	Arg	Asn	Asp	Pro	Lys	Cys	850	855	860	
Thr	Thr	Ala	Leu	Val	Ile	Ser	Gly	Ala	Ser	Trp	Glu	Thr	Tyr	Ala	Asn	865	870	875	880
Asn	Leu	Ala	Arg	Gln	Ala	Leu	Gln	Val	Arg	Ala	Gly	Ser	His	Tyr	Ala	885	890	895	
Phe	Ser	Pro	Met	Phe	Glu	Val	Leu	Gly	Gln	Phe	Val	Phe	Glu	Val	Arg	900	905	910	
Gly	Ser	Ser	Arg	Ile	Tyr	Asn	Val	Asp	Leu	Gly	Gly	Lys	Phe	Gln	Phe	915	920	925	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3052 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGCGATTTT	CGCTCTGCGG	ATTTCTCTCTA	GTTTTTTTCTT	TAACATTGCT	CTCAGTCTTC	60
GACACTTCTT	TGAGTGCTAC	TACGATTTCT	TTAACCCAG	AAGATAGTTT	TCATGGAGAT	120
AGTCAGAATG	CAGAACGTTT	TTATAATGTT	CAAGCTGGGG	ATGTCTATAG	CCTTACTGGT	180
GATGTCTCAA	TATCTAACGT	CGATAACTCT	GCATTAAATA	AAGCCTGCTT	CAATGTGACC	240
TCAGGAAGTG	TGACGTTTCG	AGGAAATCAT	CATGGGTTAT	ATTTTAAATA	TATTTCTCTA	300
GGAACACAA	AGGAAGGGGG	TGTACTTTGT	TGCCAAGATC	CTCAAGCAAC	GGCACGTTTT	360
TCTGGGTTCT	CCACGCTCTC	TTTTATTTCAG	AGCCCCGGAG	ATATTAAAGA	ACAGGGATGT	420
CTCTATTCAA	AAAATGCACT	TATGCTCTTA	AACAATTATG	TAGTGCGTTT	TGAACAAAAC	480
CAAAGTAAGA	CTAAAGGCGG	AGCTATTAGT	GGGGCGAATG	TTACTATAGT	AGGCAACTAC	540
GATTCCGTCT	CTTTCTATCA	GAATGCAGCC	ACTTTTGGAG	GTGCTATCCA	TTCTTCAGGT	600
CCCCTACAGA	TTGCAGTAAA	TCAGGCAGAG	ATAAGATTTG	CACAAAATAC	TGCCAAGAAT	660
GGTTCTGGAG	GGGCTTTGTA	CTCCGATGGT	GATATTGATA	TTGATCAGAA	TGCTTATGTT	720
CTATTTTCGAG	AAAATGAGGC	ATTGACTACT	GCTATAGGTA	AGGGAGGGGG	TGTCTGTTGT	780
CTTCCCCTT	CAGGAAGTAG	TACTCCAGTT	CCTATTGTGA	CTTTCTCTGA	CAATAAACAG	840
TTAGTCTTTG	AAAGAAACCA	TTCCATAATG	GGTGGCGGAG	CCATTTATGC	TAGGAACTT	900
AGCATCTCTT	CAGGAGGTCC	TACTCTATTT	ATCAATAATA	TATCATATGC	AAATTCGCAA	960
AATTTAGGTG	GAGCTATTGC	CATTGATACT	GGAGGGGAGA	TCAGTTTATC	AGCAGAGAAA	1020
GGAACAATTA	CATTCCAAGG	AAACCGGACG	AGCTTACCGT	TTTTGAATGG	CATCCATCTT	1080
TTACAAAATG	CTAAATTCCCT	GAAATTACAG	GCGAGAAATG	GATGCTCTAT	AGAATTTTAT	1140
GATCCTATTA	CTTCTGAAGC	AGATGGGTCT	ACCCAATTGA	ATATCAACGG	AGATCCTAAA	1200
AATAAAGAGT	ACACAGGGAC	CATACTCTTT	TCTGGAGAAA	AGAGTCTAGC	AAACGATCCT	1260
AGGGATTTTA	AATCTACAAT	CCCTCAGAAC	GTCAACCTGT	CTGCAGGATA	CTTAGTTATT	1320
AAAGAGGGGG	CCGAAGTCAC	AGTTTCAAAA	TTACGCGAGT	CTCCAGGATC	GCATTTAGTT	1380
TTAGATTTAG	GAACCAAACT	GATAGCCTCT	AAGGAAGACA	TTGCCATCAC	AGGCCTCGCG	1440
ATAGATATAG	ATAGCTTAAG	CTCATCCTCA	ACAGCAGCTG	TTATTAAAGC	AAACACCGCA	1500
AATAAACAGA	TATCCGTGAC	GGACTCTATA	GAACCTATCT	CGCCTACTGG	CAATGCCTAT	1560
GAAGATCTCA	GAATGAGAAA	TTACAGACG	TTCCCTCTGC	TCTCTTTAGA	GCCTGGAGCC	1620
GGGGGTAGTG	TGACTGTAAC	TGCTGGAGAT	TTCCCTACCG	TAAGTCCCCA	TTATGGTTTT	1680
CAAGGCAATT	GGAAATTAGC	TTGGACAGGA	ACTGGAAACA	AAGTTGGAGA	ATTCTTCTGG	1740
GATAAAATAA	ATTATAAGCC	TAGACCTGAA	AAAGAAGGAA	ATTTAGTTCC	TAATATCTTG	1800
TGGGGGAATG	CTGTAAATGT	CAGATCCTTA	ATGCAGGTTT	AAGAGACCCA	TGCATCGAGC	1860
TTACAGACAG	ATCGAGGGCT	GTGGATCGAT	GGAATTGGGA	ATTTCTTCCA	TGTATCTGCC	1920
TCCGAAGACA	ATATAAGGTA	CCGTCATAAC	AGCGGTGGAT	ATGTTCTATC	TGTAAATAAT	1980
GAGATCACAC	CTAAGCACTA	TACTTCGATG	GCATTTTCCC	AACTCTTTAG	TAGAGACAAG	2040
GACTATGCGG	TTTCCAACAA	CGAATACAGA	ATGTATTTAG	GATCGTATCT	CTATCAATAT	2100
ACAACCTCCC	TAGGGAATAT	TTTCCGTTAT	GCTTCGCGTA	ACCCTAATGT	AAACGTCGGG	2160
ATTCTCTCAA	GAAGGTTTCT	TCAAAATCCT	CTTATGATTT	TTCATTTTTT	GTGTGCTTAT	2220
GGTCATGCCA	CCAATGATAT	GAAAACAGAC	TACGCAAATT	TCCCTATGGT	GAAAAACAGC	2280
TGGAGAAACA	ATTGTTGGGC	TATAGAGTGC	GGAGGGAGCA	TGCCTCTATT	GGTATTTGAG	2340
AACGGAAGAC	TTTTCCAAGG	TGCCATCCCA	TTTATGAAAC	TACAATTAGT	TTATGCTTAT	2400
CAGGGAGATT	TCAAAGAGAC	GACTGCAGAT	GGCCGTAGAT	TTAGTAATGG	GAGTTTAAAC	2460
TCGATTTCTG	TACCTCTAGG	CATACGCTTT	GAGAAGCTGG	CACTTTCTCA	GGATGTACTC	2520
TATGACTTTA	GTTTCTCCTA	TATTCTTGAT	ATTTTCCGTA	AGGATCCCTC	ATGTGAAGCT	2580
GCTCTGGTGA	TTAGCGGAGA	CTCCTGGCTT	GTTCCGGCAG	CACACGTATC	AAGACATGCT	2640
TTTGTAGGGA	GTGGAACGGG	TCGGTATCAC	TTTAACGACT	ATACTGAGCT	CTTATGTCGA	2700
GGAAGTATAG	AATGCCGCC	CCATGCTAGG	AATTATAATA	TAAACTGTGG	AAGCAAATTT	2760
CGTTTTTAGA	AGGTTTCCAT	TGCTGTGTG	GTTCCGGATC	TTAACTATAA	ATCCTGGACT	2820

ATGGATCATA GGCATTGGGT TTCTCGAACT TGTGTGGAGA ATAACGACAT TTTATATGCA 2880
 TAACGGAATA CTCGTATCAC CTCAGCCCCT AGAGACATTC TTTAGGGGTT CTTTATTTGT 2940
 CTAAACTTCG TATTTTATCG AGAATCCTTT ACGTTCTTGG TTTGCTTGTC TCCGAGGAGT 3000
 TCTCTAACGA ATCATAGGGA TTCCAGGGTT CTGTTCTTGG AGTCCTTTGG A 3051

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 922 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Arg Phe Ser Leu Cys Gly Phe Pro Leu Val Phe Ser Leu Thr Leu
 1 5 10 15
 Leu Ser Val Phe Asp Thr Ser Leu Ser Ala Thr Thr Ile Ser Leu Thr
 20 25 30
 Pro Glu Asp Ser Phe His Gly Asp Ser Gln Asn Ala Glu Arg Ser Tyr
 35 40 45
 Asn Val Gln Ala Gly Asp Val Tyr Ser Leu Thr Gly Asp Val Ser Ile
 50 55 60
 Ser Asn Val Asp Asn Ser Ala Leu Asn Lys Ala Cys Phe Asn Val Thr
 65 70 75 80
 Ser Gly Ser Val Thr Phe Ala Gly Asn His His Gly Leu Tyr Phe Asn
 85 90 95
 Asn Ile Ser Ser Gly Thr Thr Lys Glu Gly Ala Val Leu Cys Cys Gln
 100 105 110
 Asp Pro Gln Ala Thr Ala Arg Phe Ser Gly Phe Ser Thr Leu Ser Phe
 115 120 125
 Ile Gln Ser Pro Gly Asp Ile Lys Glu Gln Gly Cys Leu Tyr Ser Lys
 130 135 140
 Asn Ala Leu Met Leu Leu Asn Asn Tyr Val Val Arg Phe Glu Gln Asn
 145 150 155 160
 Gln Ser Lys Thr Lys Gly Gly Ala Ile Ser Gly Ala Asn Val Thr Ile
 165 170 175
 Val Gly Asn Tyr Asp Ser Val Ser Phe Tyr Gln Asn Ala Ala Thr Phe
 180 185 190
 Gly Gly Ala Ile His Ser Ser Gly Pro Leu Gln Ile Ala Val Asn Gln
 195 200 205
 Ala Glu Ile Arg Phe Ala Gln Asn Thr Ala Lys Asn Gly Ser Gly Gly
 210 215 220

Ala	Leu	Tyr	Ser	Asp	Gly	Asp	Ile	Asp	Ile	Asp	Gln	Asn	Ala	Tyr	Val	225	230	235	240
Leu	Phe	Arg	Glu	Asn	Glu	Ala	Leu	Thr	Thr	Ala	Ile	Gly	Lys	Gly	Gly	245	250	255	
Ala	Val	Cys	Cys	Leu	Pro	Thr	Ser	Gly	Ser	Ser	Thr	Pro	Val	Pro	Ile	260	265	270	
Val	Thr	Phe	Ser	Asp	Asn	Lys	Gln	Leu	Val	Phe	Glu	Arg	Asn	His	Ser	275	280	285	
Ile	Met	Gly	Gly	Gly	Ala	Ile	Tyr	Ala	Arg	Lys	Leu	Ser	Ile	Ser	Ser	290	295	300	
Gly	Gly	Pro	Thr	Leu	Phe	Ile	Asn	Asn	Ile	Ser	Tyr	Ala	Asn	Ser	Gln	305	310	315	320
Asn	Leu	Gly	Gly	Ala	Ile	Ala	Ile	Asp	Thr	Gly	Gly	Glu	Ile	Ser	Leu	325	330	335	
Ser	Ala	Glu	Lys	Gly	Thr	Ile	Thr	Phe	Gln	Gly	Asn	Arg	Thr	Ser	Leu	340	345	350	
Pro	Phe	Leu	Asn	Gly	Ile	His	Leu	Leu	Gln	Asn	Ala	Lys	Phe	Leu	Lys	355	360	365	
Leu	Gln	Ala	Arg	Asn	Gly	Cys	Ser	Ile	Glu	Phe	Tyr	Asp	Pro	Ile	Thr	370	375	380	
Ser	Glu	Ala	Asp	Gly	Ser	Thr	Gln	Leu	Asn	Ile	Asn	Gly	Asp	Pro	Lys	385	390	395	400
Asn	Lys	Glu	Tyr	Thr	Gly	Thr	Ile	Leu	Phe	Ser	Gly	Glu	Lys	Ser	Leu	405	410	415	
Ala	Asn	Asp	Pro	Arg	Asp	Phe	Lys	Ser	Thr	Ile	Pro	Gln	Asn	Val	Asn	420	425	430	
Leu	Ser	Ala	Gly	Tyr	Leu	Val	Ile	Lys	Glu	Gly	Ala	Glu	Val	Thr	Val	435	440	445	
Ser	Lys	Phe	Thr	Gln	Ser	Pro	Gly	Ser	His	Leu	Val	Leu	Asp	Leu	Gly	450	455	460	
Thr	Lys	Leu	Ile	Ala	Ser	Lys	Glu	Asp	Ile	Ala	Ile	Thr	Gly	Leu	Ala	465	470	475	480
Ile	Asp	Ile	Asp	Ser	Leu	Ser	Ser	Ser	Ser	Thr	Ala	Ala	Val	Ile	Lys	485	490	495	
Ala	Asn	Thr	Ala	Asn	Lys	Gln	Ile	Ser	Val	Thr	Asp	Ser	Ile	Glu	Leu	500	505	510	
Ile	Ser	Pro	Thr	Gly	Asn	Ala	Tyr	Glu	Asp	Leu	Arg	Met	Arg	Asn	Ser	515	520	525	

Gln Thr Phe Pro Leu Leu Ser Leu Glu Pro Gly Ala Gly Gly Ser Val
 530 535 540
 Thr Val Thr Ala Gly Asp Phe Leu Pro Val Ser Pro His Tyr Gly Phe
 545 550 555 560
 Gln Gly Asn Trp Lys Leu Ala Trp Thr Gly Thr Gly Asn Lys Val Gly
 565 570 575
 Glu Phe Phe Trp Asp Lys Ile Asn Tyr Lys Pro Arg Pro Glu Lys Glu
 580 585 590
 Gly Asn Leu Val Pro Asn Ile Leu Trp Gly Asn Ala Val Asn Val Arg
 595 600 605
 Ser Leu Met Gln Val Gln Glu Thr His Ala Ser Ser Leu Gln Thr Asp
 610 615 620
 Arg Gly Leu Trp Ile Asp Gly Ile Gly Asn Phe Phe His Val Ser Ala
 625 630 635 640
 Ser Glu Asp Asn Ile Arg Tyr Arg His Asn Ser Gly Gly Tyr Val Leu
 645 650 655
 Ser Val Asn Asn Glu Ile Thr Pro Lys His Tyr Thr Ser Met Ala Phe
 660 665 670
 Ser Gln Leu Phe Ser Arg Asp Lys Asp Tyr Ala Val Ser Asn Asn Glu
 675 680 685
 Tyr Arg Met Tyr Leu Gly Ser Tyr Leu Tyr Gln Tyr Thr Thr Ser Leu
 690 695 700
 Gly Asn Ile Phe Arg Tyr Ala Ser Arg Asn Pro Asn Val Asn Val Gly
 705 710 715 720
 Ile Leu Ser Arg Arg Phe Leu Gln Asn Pro Leu Met Ile Phe His Phe
 725 730 735
 Leu Cys Ala Tyr Gly His Ala Thr Asn Asp Met Lys Thr Asp Tyr Ala
 740 745 750
 Asn Phe Pro Met Val Lys Asn Ser Trp Arg Asn Asn Cys Trp Ala Ile
 755 760 765
 Glu Cys Gly Gly Ser Met Pro Leu Leu Val Phe Glu Asn Gly Arg Leu
 770 775 780
 Phe Gln Gly Ala Ile Pro Phe Met Lys Leu Gln Leu Val Tyr Ala Tyr
 785 790 795 800
 Gln Gly Asp Phe Lys Glu Thr Thr Ala Asp Gly Arg Arg Phe Ser Asn
 805 810 815
 Gly Ser Leu Thr Ser Ile Ser Val Pro Leu Gly Ile Arg Phe Glu Lys
 820 825 830

Leu Ala Leu Ser Gln Asp Val Leu Tyr Asp Phe Ser Phe Ser Tyr Ile
 835 840 845
 Pro Asp Ile Phe Arg Lys Asp Pro Ser Cys Glu Ala Ala Leu Val Ile
 850 855 860
 Ser Gly Asp Ser Trp Leu Val Pro Ala Ala His Val Ser Arg His Ala
 865 870 875 880
 Phe Val Gly Ser Gly Thr Gly Arg Tyr His Phe Asn Asp Tyr Thr Glu
 885 890 895
 Leu Leu Cys Arg Gly Ser Ile Glu Cys Arg Pro His Ala Arg Asn Tyr
 900 905 910
 Asn Ile Asn Cys Gly Ser Lys Phe Arg Phe
 915 920

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGAAGATTC	CACTCCGCTT	TTTATTGATA	TCATTAGTAC	CTACGCTTTC	TATGTCGAAT	60
TTATTAGGAG	CTGCTACTAC	CGAAGAGCTA	TCGGCTAGCA	ATAGCTTCGA	TGGAAC TACA	120
TCAACAACAA	GCTTTTCTAG	TAAAACATCA	TCGGCTACAG	ATGGCACCAA	TTATGTTTTT	180
AAAGATTCTG	TAGTTATAGA	AAATGTACCC	AAAACAGGGG	AAACTCAGTC	TACTAGTTGT	240
TTTAAAAATG	ACGCTGCAGC	TGGAGATCTA	AATTTCTTAG	GAGGGGGATT	TTCTTTCACA	300
TTTAGCAATA	TCGATGCAAC	CACGGCTTCT	GGAGCTGCTA	TTGGAAGTGA	AGCAGCTAAT	360
AAGACAGTCA	CGTTATCAGG	ATTTTCGGCA	CTTTCTTTTC	TTAAATCCCC	AGCAAGTACA	420
GTGACTAATG	GATTGGGAGC	TATCAATGTT	AAAGGGAATT	TAAGCCTATT	GGATAATGAT	480
AAGGTATTGA	TTCAGGACAA	TTTCTCAACA	GGAGATGGCG	GAGCAATTAA	TTGTGCAGGC	540
TCCTTGAAGA	TCGCAACAA	TAAGTCCCTT	TCTTTTATTG	GAAATAGTTC	TTCAACACGT	600
GGCGGAGCGA	TTCATACCAA	AAACCTCACA	CTATCTTCTG	GTGGGGAAAC	TCTATTTTCAG	660
GGGAATACAG	CGCCTACGGC	TGCTGGTAAA	GGAGGTGCTA	TCGCGATTGC	AGACTCTGGC	720
ACCTTATCCA	TTTCTGGAGA	CAGTGGCGAC	ATTATCTTTG	AAGGCAATAC	GATAGGAGCT	780
ACAGGAACCG	TCTCTCATAG	TGCTATTGAT	TTAGGAACTA	GCGCTAAGAT	AACTGCGTTA	840
CGTGCTGCGC	AAGGACATAC	GATATACTTT	TATGATCCGA	TTACTGTAAC	AGGATCGACA	900
TCTGTTGCTG	ATGCTCTCAA	TATTAATAGC	CCTGATACTG	GAGATAACAA	AGAGTATACG	960
GGAACCATAG	TCTTTTCTGG	AGAGAAGCTC	ACGGAGGCAG	AAGCTAAAGA	TGAGAAGAAC	1020
CGCACTTCTA	AATTACTTCA	AAATGTTGCT	TTTAAAAATG	GGACTGTAGT	TTTAAAAGGT	1080
GATGTCGTTT	TAAGTGCGAA	CGGTTTCTCT	CAGGATGCAA	ACTCTAAGTT	GATTATGGAT	1140
TTAGGGACGT	CGTTGGTTGC	AAACACCGAA	AGTATCGAGT	TAACGAATTT	GGAAATTAAT	1200
ATAGACTCTC	TCAGGAACGG	GAAAAAGATA	AAACTCAGTG	CTGCCACAGC	TCAGAAAAGAT	1260
ATTCGTATAG	ATCGTCCTGT	TGTACTGGCA	ATTAGCGATG	AGAGTTTTTA	TCAAAATGGC	1320
TTTTTTGAATG	AGGACCAATC	CTATGATGGG	ATTCTTGAGT	TAGATGCTGG	GAAAGACATC	1380
GTGATTTCTG	CAGATTCTCG	CAGTATAAAT	GCTGTACAAT	CTCCGTATGG	CTATCAGGGA	1440
AAGTGGACAA	TCAATTGGTC	TACTGATGAT	AAGAAAGCTA	CGGTTTCTTG	GGCAAAGCAA	1500
AGTTTTTAATC	CCACTGCTGA	GCAGGAGGCT	CCGTTAGTTC	CTAATCTTCT	TTGGGGTTCT	1560
TTTATAGATG	TTTCGTCCCTT	CCAAAATTTT	ATAGAGCTAG	GTACTGAAGG	TGCTCCTTAC	1620
GAAAAGAGAT	TTTGGGTTGC	AGGCATTTCC	AATGTTTTGC	ATAGGAGCGG	TCGTGAAAAT	1680

```

CAAAGGAAAT TCCGTCATGT GAGTGGAGGT GCTGTAGTAG GTGCTAGCAC GAGGATGCCG 1740
GGTGGTGATA CCTTGTCTCT GGGTTTTGCT CAGCTCTTTG CGCGTGACAA AGACTACTTT 1800
ATGAATACCA ATTTTCGAAA GACCTACGCA GGATCTTTAC GTTTGCAGCA CGATGCTTCC 1860
CTATACTCTG TGGTGAGTAT CCTTTTAGGA GAGGGAGGAC TCCGCGAGAT CCTGTTGCCT 1920
TATGTTTCCA AGACTCTGCC GTGCTCTTTC TATGGGCAGC TTAGCTACGG CCATACGGAT 1980
CATCGCATGA AGACCGAGTC TCTACCCCCC CCCCCCCC GA GCTCTCGAC GGATCATACT 2040
TCTTGGGGAG GATATGTCTG GGCTGGAGAG CTGGGAACTC GAGTTGCTGT TGAAAATACC 2100
AGCGGCAGAG GATTTTTCCG AGAGTACACT CCATTTGTAA AAGTCCAAGC TGTTTACTCG 2160
CGCCAAGATA GCTTTGTTGA ACTAGGAGCT ATCAGTCGTG ATTTTAGTGA TTCGCATCTT 2220
TATAACCTTG CGATTCTCTT TGAATCAAG TTAGAGAAAC GGTTCGAGA GCAATATTAT 2280
CATGTTGTAG CGATGTATTC TCCAGATGTT TGTCGTAGTA ACCCCAAATG TACGACTACC 2340
CTACTTTCCA ACCAAGGGAG TTGGAAGACC AAAGGTTTCA ACTTAGCAAG ACAGGCTGGT 2400
ATTGTTTCAAG CCTCAGGTTT TCGATCTTTG GGAGCTGCAG CAGAGCTTTT CGGGAACCTT 2460
GGCTTTGAAT GCGGGGGATC TTCTCGTAGC TATAATGTAG ATGCGGGTAG CAAAATCAAA 2520
TTTTAG

```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

Met Lys Ile Pro Leu Arg Phe Leu Leu Ile Ser Leu Val Pro Thr Leu
 1             5             10             15

Ser Met Ser Asn Leu Leu Gly Ala Ala Thr Thr Glu Glu Leu Ser Ala
          20             25             30

Ser Asn Ser Phe Asp Gly Thr Thr Ser Thr Thr Ser Phe Ser Ser Lys
          35             40             45

Thr Ser Ser Ala Thr Asp Gly Thr Asn Tyr Val Phe Lys Asp Ser Val
          50             55             60

Val Ile Glu Asn Val Pro Lys Thr Gly Glu Thr Gln Ser Thr Ser Cys
          65             70             75             80

Phe Lys Asn Asp Ala Ala Ala Gly Asp Leu Asn Phe Leu Gly Gly Gly
          85             90             95

Phe Ser Phe Thr Phe Ser Asn Ile Asp Ala Thr Thr Ala Ser Gly Ala
          100            105            110

Ala Ile Gly Ser Glu Ala Ala Asn Lys Thr Val Thr Leu Ser Gly Phe
          115            120            125

Ser Ala Leu Ser Phe Leu Lys Ser Pro Ala Ser Thr Val Thr Asn Gly
          130            135            140

Leu Gly Ala Ile Asn Val Lys Gly Asn Leu Ser Leu Leu Asp Asn Asp
          145            150            155            160

```

Lys Val Leu Ile Gln Asp Asn Phe Ser Thr Gly Asp Gly Gly Ala Ile
 165 170 175
 Asn Cys Ala Gly Ser Leu Lys Ile Ala Asn Asn Lys Ser Leu Ser Phe
 180 185 190
 Ile Gly Asn Ser Ser Ser Thr Arg Gly Gly Ala Ile His Thr Lys Asn
 195 200 205
 Leu Thr Leu Ser Ser Gly Gly Glu Thr Leu Phe Gln Gly Asn Thr Ala
 210 215 220
 Pro Thr Ala Ala Gly Lys Gly Gly Ala Ile Ala Ile Ala Asp Ser Gly
 225 230 235 240
 Thr Leu Ser Ile Ser Gly Asp Ser Gly Asp Ile Ile Phe Glu Gly Asn
 245 250 255
 Thr Ile Gly Ala Thr Gly Thr Val Ser His Ser Ala Ile Asp Leu Gly
 260 265 270
 Thr Ser Ala Lys Ile Thr Ala Leu Arg Ala Ala Gln Gly His Thr Ile
 275 280 285
 Tyr Phe Tyr Asp Pro Ile Thr Val Thr Gly Ser Thr Ser Val Ala Asp
 290 295 300
 Ala Leu Asn Ile Asn Ser Pro Asp Thr Gly Asp Asn Lys Glu Tyr Thr
 305 310 315 320
 Gly Thr Ile Val Phe Ser Gly Glu Lys Leu Thr Glu Ala Glu Ala Lys
 325 330 335
 Asp Glu Lys Asn Arg Thr Ser Lys Leu Leu Gln Asn Val Ala Phe Lys
 340 345 350
 Asn Gly Thr Val Val Leu Lys Gly Asp Val Val Leu Ser Ala Asn Gly
 355 360 365
 Phe Ser Gln Asp Ala Asn Ser Lys Leu Ile Met Asp Leu Gly Thr Ser
 370 375 380
 Leu Val Ala Asn Thr Glu Ser Ile Glu Leu Thr Asn Leu Glu Ile Asn
 385 390 395 400
 Ile Asp Ser Leu Arg Asn Gly Lys Lys Ile Lys Leu Ser Ala Ala Thr
 405 410 415
 Ala Gln Lys Asp Ile Arg Ile Asp Arg Pro Val Val Leu Ala Ile Ser
 420 425 430
 Asp Glu Ser Phe Tyr Gln Asn Gly Phe Leu Asn Glu Asp His Ser Tyr
 435 440 445
 Asp Gly Ile Leu Glu Leu Asp Ala Gly Lys Asp Ile Val Ile Ser Ala
 450 455 460

Asp	Ser	Arg	Ser	Ile	Asn	Ala	Val	Gln	Ser	Pro	Tyr	Gly	Tyr	Gln	Gly	465	470	475	480
Lys	Trp	Thr	Ile	Asn	Trp	Ser	Thr	Asp	Asp	Lys	Lys	Ala	Thr	Val	Ser	485	490		495
Trp	Ala	Lys	Gln	Ser	Phe	Asn	Pro	Thr	Ala	Glu	Gln	Glu	Ala	Pro	Leu	500	505		510
Val	Pro	Asn	Leu	Leu	Trp	Gly	Ser	Phe	Ile	Asp	Val	Arg	Pro	Phe	Gln	515	520		525
Asn	Phe	Ile	Glu	Leu	Gly	Thr	Glu	Gly	Ala	Pro	Tyr	Glu	Lys	Arg	Phe	530	535		540
Trp	Val	Ala	Gly	Ile	Ser	Asn	Val	Leu	His	Arg	Ser	Gly	Arg	Glu	Asn	545	550	555	560
Gln	Arg	Lys	Phe	Arg	His	Val	Ser	Gly	Gly	Ala	Val	Val	Gly	Ala	Ser	565	570		575
Thr	Arg	Met	Pro	Gly	Gly	Asp	Thr	Leu	Ser	Leu	Gly	Phe	Ala	Gln	Leu	580	585		590
Phe	Ala	Arg	Asp	Lys	Asp	Tyr	Phe	Met	Asn	Thr	Asn	Phe	Ala	Lys	Thr	595	600		605
Tyr	Ala	Gly	Ser	Leu	Arg	Leu	Gln	His	Asp	Ala	Ser	Leu	Tyr	Ser	Val	610	615		620
Val	Ser	Ile	Leu	Leu	Gly	Glu	Gly	Gly	Leu	Arg	Glu	Ile	Leu	Leu	Pro	625	630	635	640
Tyr	Val	Ser	Lys	Thr	Leu	Pro	Cys	Ser	Phe	Tyr	Gly	Gln	Leu	Ser	Tyr	645	650		655
Gly	His	Thr	Asp	His	Arg	Met	Lys	Thr	Glu	Ser	Leu	Pro	Pro	Pro	Pro	660	665		670
Pro	Thr	Leu	Ser	Thr	Asp	His	Thr	Ser	Trp	Gly	Gly	Tyr	Val	Trp	Ala	675	680		685
Gly	Glu	Leu	Gly	Thr	Arg	Val	Ala	Val	Glu	Asn	Thr	Ser	Gly	Arg	Gly	690	695	700	
Phe	Phe	Arg	Glu	Tyr	Thr	Pro	Phe	Val	Lys	Val	Gln	Ala	Val	Tyr	Ser	705	710	715	720
Arg	Gln	Asp	Ser	Phe	Val	Glu	Leu	Gly	Ala	Ile	Ser	Arg	Asp	Phe	Ser	725	730		735
Asp	Ser	His	Leu	Tyr	Asn	Leu	Ala	Ile	Pro	Leu	Gly	Ile	Lys	Leu	Glu	740	745		750
Lys	Arg	Phe	Ala	Glu	Gln	Tyr	Tyr	His	Val	Val	Ala	Met	Tyr	Ser	Pro	755	760		765

Asp Val Cys Arg Ser Asn Pro Lys Cys Thr Thr Thr Leu Leu Ser Asn
 770 775 780
 Gln Gly Ser Trp Lys Thr Lys Gly Ser Asn Leu Ala Arg Gln Ala Gly
 785 790 795 800
 Ile Val Gln Ala Ser Gly Phe Arg Ser Leu Gly Ala Ala Ala Glu Leu
 805 810 815
 Phe Gly Asn Phe Gly Phe Glu Trp Arg Gly Ser Ser Arg Ser Tyr Asn
 820 825 830
 Val Asp Ala Gly Ser Lys Ile Lys Phe
 835 840

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAAGTCTT	CTTTCCCCAA	GTTTGTATTT	TCTACATTTG	CTATTTTCCC	TTTGTCTATG	60
ATTGCTACCG	AGACAGTTTT	GGATTCAAGT	GCGAGTTTCG	ATGGGAATAA	AAATGGTAAT	120
TTTTTCAGTTC	GTGAGAGTCA	GGAAGATGCT	GGAACACCT	ACCTATTTAA	GGGAAATGTC	180
ACTCTAGAAA	ATATTCCTGG	AACAGGCACA	GCAATCACAA	AAAGCTGTTT	TAACAACACT	240
AAGGGCGATT	TGACTTTTAC	AGGTAACGGG	AACCTCTCTAT	TGTTCCAAAC	GGTGGATGCA	300
GGGACTGTAG	CAGGGGCTGC	TGTTAACAGC	AGCGTGGTAG	ATAAATCTAC	CACGTTTATA	360
GGGTTTTCTT	CGCTATCTTT	TATTGCGTCT	CCTGGAAGTT	CGATAACTAC	CGGCAAAGGA	420
GCCGTTAGCT	GCTCTACGGG	TAGCTTGAAG	TTTGACAAAA	ATGTCAGTTT	GCTCTTCAGC	480
AAAAACTTTT	CAACGGATAA	TGGCGGTGCT	ATCACCGCAA	AAACTCTTTC	ATTAACAGGG	540
ACTACAATGT	CAGCTCTGTT	TTCTGAAAAT	ACCTCCTCAA	AGAAAGGCGG	AGCCATTCAG	600
ACTTCCGATG	CCCTTACCAT	TACTGGAAAC	CAAGGGGAAG	TCTCTTTTTC	TGACAATACT	660
TCTTCGGATT	CTGGAGCTGC	AATTTTACA	GAAGCCTCGG	TGACTATTTT	TAATAATGCT	720
AAAGTTTCCT	TTATTGACAA	TAAGGTCACA	GGAGCGAGCT	CCTCAACAAC	GGGGGATATG	780
TCAGGAGGTG	CTATCTGTGC	TTATAAAACT	AGTACAGATA	CTAAGGTCAC	CCTCACTGGA	840
AATCAGATGT	TACTCTTCAG	CAACAATACA	TCGACAACAG	CGGGAGGAGC	TATCTATGTG	900
AAAAAGCTCG	AACTGGCTTC	CGGAGGACTT	ACCCTATTCA	GTAGAAATAG	TGTCAATGGA	960
GGTACAGCTC	CTAAAGGTGG	AGCCATAGCT	ATCGAAGATA	GTGGGGAATT	GAGTTTATCC	1020
GCCGATAGTG	GTGACATTGT	CTTTTATAGG	AATACAGTCA	CTTCTACTAC	TCCTGGGACG	1080
AATAGAAGTA	GTATCGACTT	AGGAACGAGT	GCAAAGATGA	CAGCTTTGCG	TTCTGCTGCT	1140
GGTAGAGCCA	TCTACTTCTA	TGATCCCATA	ACTACAGGAT	CTTCCACAAC	AGTTACAGAT	1200
GTCTTAAAAG	TTAATGAGAC	TCCGGCAGAT	TCTGCACTAC	AATATACAGG	GAACATCATC	1260
TTACAGGAG	AAAAGTTATC	AGAGACAGAG	GCCGCAGATT	CTAAAAATCT	TACTTCGAAG	1320
CTACTACAGC	CTGTAACTCT	TTCAGGAGGT	ACTCTATCTT	TAAAACATGG	AGTGACTCTG	1380
CAGACTCAGG	CATTCACTCA	ACAGGCAGAT	TCTCGTCTCG	AAATGGACGT	AGGAACTACT	1440
CTAGAACCTG	CTGATACTAG	CACCATAAAC	AATTTGGTCA	TTAACATCAG	TTCTATAGAC	1500
GGTGCAAGA	AGGCAAAAAT	AGAAACCAAA	GACTCGTCAA	AAAATCTGAC	TTTATCTGGA	1560
ACCATCATTT	TATTGGACCC	GACGGGCACG	TTTTATGAAA	ATCATAGTTT	AAGAAATCCT	1620
CAGTCCTACG	ACATCTTAGA	GCTCAAAGCT	TCTGGAAGCT	TAACAAGCAC	CGCAGTGACT	1680
CCAGATCCTA	TAATGGGTGA	GAAATTCCAT	TACGGCTATC	AGGGAACTTG	GGGCCCCAAT	1740
GTTTGGGGGA	CAGGGGCTTC	TACGACTGCA	ACCTTCAACT	GGACTAAAAC	TGGCTATATT	1800
CCTAATCCCG	AGCGTATCGG	CTCTTTAGTC	CCTAATAGCT	TATGGAATGC	ATTTATAGAT	1860

```

ATTAGCTCTC TCCATTATCT TATGGAGACT GCAAACGAAG GGTTCAGGG AGACCGTGCT 1920
TTTTGGTGTG CTGGATTATC TAACTTCTTC CATAAGGATA GTACAAAAAC ACGACGCGGG 1980
TTTCGCCATT TGAGTGGCGG TTATGTCATA GGAGGAAACC TACATACTTG TTCAGATAAG 2040
ATTCTTAGTG CTGCATTTTG TCAGCTCTTT GGAAGAGATA GAGACTACTT TGTAGCTAAG 2100
AATCAAGGTA CAGTCTACGG AGGAACCTCTC TATTACCAGC ACAACGAAAC CTATATCTCT 2160
CTTCCTTGCA AACTACGGCC TTGTTTCGTTG TCTTATGTTT CTACAGAGAT TCCTGTTCTC 2220
TTTTCAGGAA ACCTTAGCTA CACCCATACG GATAACGATC TGAAAACCAA GTATACAACA 2280
TATCCTACTG TTAAAGGAAG CTGGGGGAAT GATAGTTTCG CTTTAGAATT CGGTGGAAGA 2340
GCTCCGATTT GCTTAGATGA AAGTGCTCTA TTTGAGCAGT ACATGCCCTT CATGAAATTG 2400
CAGTTTGTCT ATGCACATCA GGAAGGTTTT AAAGAACAGG GAACAGAAGC TCGTGAATTT 2460
GGAAGTAGCC GTCTTGTA TCTTGCCTTA CCTATCGGGA TCCGATTGTA TAAGGAATCA 2520
GACTGCCAAG ATGCAACGTA CAATCTAACT CTTGGTTATA CTGTGGATCT TGTTCGTAGT 2580
AACCCCGACT GTACGACAAC ACTGCGAATT AGCGGTGATT CTTGGAAAAC CTTCGGTACG 2640
AATTTGGCAA GACAAGCTTT AGTCCTTCGT GCAGGGAACC ATTTTGTCTT TAACTCAAAT 2700
TTTGAAGCCT TTAGCCAATT TTCTTTTGAA TTGCGTGGGT CATCTCGCAA TTACAATGTA 2760
GACTTAGGAG CAAAATACCA ATTCTAA 2787

```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

Met Lys Ser Ser Phe Pro Lys Phe Val Phe Ser Thr Phe Ala Ile Phe
 1             5             10             15

Pro Leu Ser Met Ile Ala Thr Glu Thr Val Leu Asp Ser Ser Ala Ser
      20             25             30

Phe Asp Gly Asn Lys Asn Gly Asn Phe Ser Val Arg Glu Ser Gln Glu
      35             40             45

Asp Ala Gly Thr Thr Tyr Leu Phe Lys Gly Asn Val Thr Leu Glu Asn
      50             55             60

Ile Pro Gly Thr Gly Thr Ala Ile Thr Lys Ser Cys Phe Asn Asn Thr
      65             70             75             80

Lys Gly Asp Leu Thr Phe Thr Gly Asn Gly Asn Ser Leu Leu Phe Gln
      85             90             95

Thr Val Asp Ala Gly Thr Val Ala Gly Ala Ala Val Asn Ser Ser Val
      100            105            110

Val Asp Lys Ser Thr Thr Phe Ile Gly Phe Ser Ser Leu Ser Phe Ile
      115            120            125

Ala Ser Pro Gly Ser Ser Ile Thr Thr Gly Lys Gly Ala Val Ser Cys
      130            135            140

Ser Thr Gly Ser Leu Lys Phe Asp Lys Asn Val Ser Leu Leu Phe Ser
      145            150            155            160

```

Lys Asn Phe Ser Thr Asp Asn Gly Gly Ala Ile Thr Ala Lys Thr Leu
 165 170 175
 Ser Leu Thr Gly Thr Thr Met Ser Ala Leu Phe Ser Glu Asn Thr Ser
 180 185 190
 Ser Lys Lys Gly Gly Ala Ile Gln Thr Ser Asp Ala Leu Thr Ile Thr
 195 200 205
 Gly Asn Gln Gly Glu Val Ser Phe Ser Asp Asn Thr Ser Ser Asp Ser
 210 215 220
 Gly Ala Ala Ile Phe Thr Glu Ala Ser Val Thr Ile Ser Asn Asn Ala
 225 230 235 240
 Lys Val Ser Phe Ile Asp Asn Lys Val Thr Gly Ala Ser Ser Ser Thr
 245 250 255
 Thr Gly Asp Met Ser Gly Gly Ala Ile Cys Ala Tyr Lys Thr Ser Thr
 260 265 270
 Asp Thr Lys Val Thr Leu Thr Gly Asn Gln Met Leu Leu Phe Ser Asn
 275 280 285
 Asn Thr Ser Thr Thr Ala Gly Gly Ala Ile Tyr Val Lys Lys Leu Glu
 290 295 300
 Leu Ala Ser Gly Gly Leu Thr Leu Phe Ser Arg Asn Ser Val Asn Gly
 305 310 315 320
 Gly Thr Ala Pro Lys Gly Gly Ala Ile Ala Ile Glu Asp Ser Gly Glu
 325 330 335
 Leu Ser Leu Ser Ala Asp Ser Gly Asp Ile Val Phe Leu Gly Asn Thr
 340 345 350
 Val Thr Ser Thr Thr Pro Gly Thr Asn Arg Ser Ser Ile Asp Leu Gly
 355 360 365
 Thr Ser Ala Lys Met Thr Ala Leu Arg Ser Ala Ala Gly Arg Ala Ile
 370 375 380
 Tyr Phe Tyr Asp Pro Ile Thr Thr Gly Ser Ser Thr Thr Val Thr Asp
 385 390 395 400
 Val Leu Lys Val Asn Glu Thr Pro Ala Asp Ser Ala Leu Gln Tyr Thr
 405 410 415
 Gly Asn Ile Ile Phe Thr Gly Glu Lys Leu Ser Glu Thr Glu Ala Ala
 420 425 430
 Asp Ser Lys Asn Leu Thr Ser Lys Leu Leu Gln Pro Val Thr Leu Ser
 435 440 445
 Gly Gly Thr Leu Ser Leu Lys His Gly Val Thr Leu Gln Thr Gln Ala
 450 455 460

Phe	Thr	Gln	Gln	Ala	Asp	Ser	Arg	Leu	Glu	Met	Asp	Val	Gly	Thr	Thr	
465					470					475						480
Leu	Glu	Pro	Ala	Asp	Thr	Ser	Thr	Ile	Asn	Asn	Leu	Val	Ile	Asn	Ile	
				485					490					495		
Ser	Ser	Ile	Asp	Gly	Ala	Lys	Lys	Ala	Lys	Ile	Glu	Thr	Lys	Ala	Thr	
			500					505					510			
Ser	Lys	Asn	Leu	Thr	Leu	Ser	Gly	Thr	Ile	Thr	Leu	Leu	Asp	Pro	Thr	
		515					520					525				
Gly	Thr	Phe	Tyr	Glu	Asn	His	Ser	Leu	Arg	Asn	Pro	Gln	Ser	Tyr	Asp	
	530					535					540					
Ile	Leu	Glu	Leu	Lys	Ala	Ser	Gly	Thr	Val	Thr	Ser	Thr	Ala	Val	Thr	
545					550					555					560	
Pro	Asp	Pro	Ile	Met	Gly	Glu	Lys	Phe	His	Tyr	Gly	Tyr	Gln	Gly	Thr	
				565					570					575		
Trp	Gly	Pro	Ile	Val	Trp	Gly	Thr	Gly	Ala	Ser	Thr	Thr	Ala	Thr	Phe	
			580					585					590			
Asn	Trp	Thr	Lys	Thr	Gly	Tyr	Ile	Pro	Asn	Pro	Glu	Arg	Ile	Gly	Ser	
		595					600					605				
Leu	Val	Pro	Asn	Ser	Leu	Trp	Asn	Ala	Phe	Ile	Asp	Ile	Ser	Ser	Leu	
	610					615					620					
His	Tyr	Leu	Met	Glu	Thr	Ala	Asn	Glu	Gly	Leu	Gln	Gly	Asp	Arg	Ala	
625					630					635					640	
Phe	Trp	Cys	Ala	Gly	Leu	Ser	Asn	Phe	Phe	His	Lys	Asp	Ser	Thr	Lys	
				645					650					655		
Thr	Arg	Arg	Gly	Phe	Arg	His	Leu	Ser	Gly	Gly	Tyr	Val	Ile	Gly	Gly	
			660					665					670			
Asn	Leu	His	Thr	Cys	Ser	Asp	Lys	Ile	Leu	Ser	Ala	Ala	Phe	Cys	Gln	
		675					680					685				
Leu	Phe	Gly	Arg	Asp	Arg	Asp	Tyr	Phe	Val	Ala	Lys	Asn	Gln	Gly	Thr	
	690					695					700					
Val	Tyr	Gly	Gly	Thr	Leu	Tyr	Tyr	Gln	His	Asn	Glu	Thr	Tyr	Ile	Ser	
705					710					715					720	
Leu	Pro	Cys	Lys	Leu	Arg	Pro	Cys	Ser	Leu	Ser	Tyr	Val	Pro	Thr	Glu	
				725					730					735		
Ile	Pro	Val	Leu	Phe	Ser	Gly	Asn	Leu	Ser	Tyr	Thr	His	Thr	Asp	Asn	
			740					745					750			
Asp	Leu	Lys	Thr	Lys	Tyr	Thr	Thr	Tyr	Pro	Thr	Val	Lys	Gly	Ser	Trp	
		755					760						765			

Gly Asn Asp Ser Phe Ala Leu Glu Phe Gly Gly Arg Ala Pro Ile Cys
 770 775 780
 Leu Asp Glu Ser Ala Leu Phe Glu Gln Tyr Met Pro Phe Met Lys Leu
 785 790 795 800
 Gln Phe Val Tyr Ala His Gln Glu Gly Phe Lys Glu Gln Gly Thr Glu
 805 810 815
 Ala Arg Glu Phe Gly Ser Ser Arg Leu Val Asn Leu Ala Leu Pro Ile
 820 825 830
 Gly Ile Arg Phe Asp Lys Glu Ser Asp Cys Gln Asp Ala Thr Tyr Asn
 835 840 845
 Leu Thr Leu Gly Tyr Thr Val Asp Leu Val Arg Ser Asn Pro Asp Cys
 850 855 860
 Thr Thr Thr Leu Arg Ile Ser Gly Asp Ser Trp Lys Thr Phe Gly Thr
 865 870 875 880
 Asn Leu Ala Arg Gln Ala Leu Val Leu Arg Ala Gly Asn His Phe Cys
 885 890 895
 Phe Asn Ser Asn Phe Glu Ala Phe Ser Gln Phe Ser Phe Glu Leu Arg
 900 905 910
 Gly Ser Ser Arg Asn Tyr Asn Val Asp Leu Gly Ala Lys Tyr Gln Phe
 915 920 925

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2757 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGAGATCGT	CTTTTTCCTT	GTTATTAATA	TCTTCATCTC	TAGCCTTTCC	TCTCTTAATG	60
AGTGTTCCTG	CAGATGCTGC	CGATCTCACA	TTAGGGAGTC	GTGACAGTTA	TAATGGTGAT	120
ACAAGCACCA	CAGAATTTAC	TCCTAAAGCG	GCAACTTCTG	ATGCTAGTGG	CACGACCTAT	180
ATTCTCGATG	GGGATGTCTC	GATAAGCCAA	GCAGGGAAAC	AAACGAGCTT	AACCACAAGT	240
TGTTTTTCTA	ACACTGCAGG	AAATCTTACC	TTCTTAGGGA	ACGGATTTTC	TCTTCATTTT	300
GACAATATTA	TTTCGTCTAC	TGTTGCAGGT	GTTGTTGTTA	GCAATACAGC	AGCTTCTGGG	360
ATTACGAAAT	TCTCAGGATT	TTCAACTCTT	CGGATGCTTG	CAGCTCCTAG	GACCACAGGT	420
AAAGGAGCCA	TTAAAATTAC	CGATGGTCTG	GTGTTTGAGA	GTATAGGGAA	TCTTGACCAA	480
AATGAAAATG	CCTCTAGTGA	AAATGGGGGA	GCCATCAATA	CGAAGACTTT	GTCTTTGACT	540
GGGAGTACGC	GGTTTGTAGC	GTTCCTTGCC	AATAGCTCGT	CGCAACAAGG	GGGAGCGATC	600
TATGCTTCTG	GTGACTCTGT	GATTTCTGAG	AATGCAGGAA	TCTTGAGCTT	CGGAAACAAC	660
AGTGCACAAA	CATCAGGAGG	CGCGATCTCT	GCTGAAGGGA	ACCTTGATGAT	CTCCAATAAC	720
CAAAATATCT	TTTTTCGATG	CTGCAAAGCA	ACTACAAATG	GCGGAGCTAT	TGATTGTAAC	780
AAAGCAGGGG	CGAACCCAGA	CCCTATCTTG	ACTCTTTCAG	GAAATGAGAG	CCTGCATTTT	840
CTGAATAACA	CAGCAGGAAA	TAGTGGAGGT	GCGATTTATA	CCAAAAAATT	GGTGTATATCC	900
TCAGGACGAG	GAGGAGTGTT	ATTTTCTAAC	AACAAAGCTG	CGAATGCTAC	TCCTAAAGGA	960

GGGGCAATTG	CGATTCTAGA	TTCTGGAGAG	ATTAGCATTT	CTGCAGATCT	CGGCAATATC	1020
ATTTTCGAGG	GCAATACTAC	GAGCACTACA	GGAAGTCCTG	CGAGTGTGAC	CAGAAATGCT	1080
ATAGATCTTG	CATCGAATGC	AAAATTTTTA	AATCTCCGAG	CGACTCGGGG	AAATAAAGTT	1140
ATTTTCTATG	ATCCTATCAC	GAGCTCAGGA	GCTACTGATA	AGCTCTCTTT	GAATAAAGCT	1200
GACGCAGGAT	CTGGAAATAC	CTATGAAGGC	TACATCGTTT	TCTCTGGAGA	GAAACTCTCA	1260
GAAGAGGAAC	TTAAGAAACC	TGACAATCTG	AAGTCTACAT	TTACACAGGC	TGTAGAGCTT	1320
GCTGCAGGTG	CCTTAGTATT	GAAAGATGGA	GTGACTGTAG	TTGCAAATAC	TATAACGCAG	1380
GTCGAGGGAT	CGAAAGTCGT	TATGGATGGA	GGGACTACTT	TTGAGGCAAG	CGCTGAGGGG	1440
GTCACCTCTCA	ATGGCCTAGC	CATTAATATA	GATTCCTTAG	ATGGGACAAA	TAAAGCTATC	1500
ATTAAGGCGA	CGGCAGCAAG	TAAGGATGTT	GCCTTATCAG	GGCCTATCAT	GCTTGTAGAT	1560
GCTCAGGGGA	ACTATTATGA	GCATCATAAT	CTCAGTCAAC	AGCAGGTCTT	TCCTTTAATA	1620
GAGCTTTCTG	CACAAGGAAC	GATGACTACT	ACAGATATCC	CCGATACCCC	AATTCTAAAT	1680
ACTACGAATC	ACTATGGGTA	TCAAGGAACT	GGAATAATTG	TTTGGGTCGA	CGATGCAACT	1740
GCAAAAACAA	AAAATGCTAC	CTTAAC TTGG	ACTAAAACAG	GATACAAGCC	GAATCCAGAA	1800
CGTCAGGGAC	CTTTGGTTCC	TAATAGCCTG	TGGGGTTCTT	TTGTGCGATG	CCGCTCCATT	1860
CAGAGCCTCA	TGGACCGGAG	CACAAGTTCG	TTATCTTCGT	CAACAAATTT	GTGGGTATCA	1920
GGAATCGCGG	ACTTTTTGCA	TGAAGATCAG	AAAGGAAACC	AACGTAGTTA	TCGTCAATTCT	1980
AGCGCGGGTT	ATGCATTAGG	AGGAGGATTC	TTCACGGCTT	CTGAAAATTT	CTTTAATTTT	2040
GCTTTTTGTC	AGCTTTTTTG	CTACGACAAG	GACCATCTTG	TGGCTAAGAA	CCATACCCAT	2100
GTATATGCAG	GGGCAATGAG	TTACCGACAC	CTCGGAGAGT	CTAAGACCCT	CGCTAAGATT	2160
TTGTCAGGAA	ATTCTGACTC	CCTACCTTTT	GTCTTCAATG	CTCGGTTTGC	TTATGGCCAT	2220
ACCGACAATA	ACATGACCAC	AAAGTACACT	GGCTATTCTC	CTGTTAAGGG	AAGCTGGGGA	2280
AATGATGCCT	TCGGTATAGA	ATGTGGAGGA	GCTATCCCGG	TAGTTGCTTC	AGGACGTCGG	2340
TCTTGGGTGG	ATACCCACAC	GCCATTTCTA	AACCTAGAGA	TGATCTATGC	ACATCAGAAT	2400
GACTTTAAGG	AAAACGGCAC	AGAAGGCCGT	TCTTTCCAAA	GTGAAGACCT	CTTCAATCTA	2460
CGGGTTCCTG	TAGGGATAAA	ATTTGAGAAA	TTCTCCGATA	AGTCTACGTA	TGATCTCTCC	2520
ATAGCTTACG	TTCCCGATGT	GATTCGTAAT	GATCCAGGCT	GCACGACAAC	TCTTATGGTT	2580
TCTGGGGATT	CTTGGTCGAC	ATGTGGTACA	AGCTTGCTTA	GACAAGCTCT	TCTTGACGT	2640
GCTGGAAATC	ATCATGCCTT	TGCTTCAAAC	TTTGAAGTTT	TCAGTCAGTT	TGAAGTCGAG	2700
TTGCGAGGTT	CTTCTCGTAG	CTATGCTATC	GATCTTGAGG	GAAGATTCGG	ATTTTAA	2757

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Arg	Ser	Ser	Phe	Ser	Leu	Leu	Leu	Ile	Ser	Ser	Ser	Leu	Ala	Phe
1				5					10					15	
Pro	Leu	Leu	Met	Ser	Val	Ser	Ala	Asp	Ala	Ala	Asp	Leu	Thr	Leu	Gly
			20					25					30		
Ser	Arg	Asp	Ser	Tyr	Asn	Gly	Asp	Thr	Ser	Thr	Thr	Glu	Phe	Thr	Pro
		35				40						45			
Lys	Ala	Ala	Thr	Ser	Asp	Ala	Ser	Gly	Thr	Thr	Tyr	Ile	Leu	Asp	Gly
	50					55					60				
Asp	Val	Ser	Ile	Ser	Gln	Ala	Gly	Lys	Gln	Thr	Ser	Leu	Thr	Thr	Ser
65					70					75					80

Cys Phe Ser Asn Thr Ala Gly Asn Leu Thr Phe Leu Gly Asn Gly Phe
 85 90 95
 Ser Leu His Phe Asp Asn Ile Ile Ser Ser Thr Val Ala Gly Val Val
 100 105 110
 Val Ser Asn Thr Ala Ala Ser Gly Ile Thr Lys Phe Ser Gly Phe Ser
 115 120 125
 Thr Leu Arg Met Leu Ala Ala Pro Arg Thr Thr Gly Lys Gly Ala Ile
 130 135 140
 Lys Ile Thr Asp Gly Leu Val Phe Glu Ser Ile Gly Asn Leu Asp Gln
 145 150 155 160
 Asn Glu Asn Ala Ser Ser Glu Asn Gly Gly Ala Ile Asn Thr Lys Thr
 165 170 175
 Leu Ser Leu Thr Gly Ser Thr Arg Phe Val Ala Phe Leu Gly Asn Ser
 180 185 190
 Ser Ser Gln Gln Gly Gly Ala Ile Tyr Ala Ser Gly Asp Ser Val Ile
 195 200 205
 Ser Glu Asn Ala Gly Ile Leu Ser Phe Gly Asn Asn Ser Ala Thr Thr
 210 215 220
 Ser Gly Gly Ala Ile Ser Ala Glu Gly Asn Leu Val Ile Ser Asn Asn
 225 230 235 240
 Gln Asn Ile Phe Phe Asp Gly Cys Lys Ala Thr Thr Asn Gly Gly Ala
 245 250 255
 Ile Asp Cys Asn Lys Ala Gly Ala Asn Pro Asp Pro Ile Leu Thr Leu
 260 265 270
 Ser Gly Asn Glu Ser Leu His Phe Leu Asn Asn Thr Ala Gly Asn Ser
 275 280 285
 Gly Gly Ala Ile Tyr Thr Lys Lys Leu Val Leu Ser Ser Gly Arg Gly
 290 295 300
 Gly Val Leu Phe Ser Asn Asn Lys Ala Ala Asn Ala Thr Pro Lys Gly
 305 310 315 320
 Gly Ala Ile Ala Ile Leu Asp Ser Gly Glu Ile Ser Ile Ser Ala Asp
 325 330 335
 Leu Gly Asn Ile Ile Phe Glu Gly Asn Thr Thr Ser Thr Thr Gly Ser
 340 345 350
 Pro Ala Ser Val Thr Arg Asn Ala Ile Asp Leu Ala Ser Asn Ala Lys
 355 360 365
 Phe Leu Asn Leu Arg Ala Thr Arg Gly Asn Lys Val Ile Phe Tyr Asp
 370 375 380

Pro Ile Thr Ser Ser Gly Ala Thr Asp Lys Leu Ser Leu Asn Lys Ala
 385 390 395 400
 Asp Ala Gly Ser Gly Asn Thr Tyr Glu Gly Tyr Ile Val Phe Ser Gly
 405 410 415
 Glu Lys Leu Ser Glu Glu Glu Leu Lys Lys Pro Asp Asn Leu Lys Ser
 420 425 430
 Thr Phe Thr Gln Ala Val Glu Leu Ala Ala Gly Ala Leu Val Leu Lys
 435 440 445
 Asp Gly Val Thr Val Val Ala Asn Thr Ile Thr Gln Val Glu Gly Ser
 450 455 460
 Lys Val Val Met Asp Gly Gly Thr Thr Phe Glu Ala Ser Ala Glu Gly
 465 470 475 480
 Val Thr Leu Asn Gly Leu Ala Ile Asn Ile Asp Ser Leu Asp Gly Thr
 485 490 495
 Asn Lys Ala Ile Ile Lys Ala Thr Ala Ala Ser Lys Asp Val Ala Leu
 500 505 510
 Ser Gly Pro Ile Met Leu Val Asp Ala Gln Gly Asn Tyr Tyr Glu His
 515 520 525
 His Asn Leu Ser Gln Gln Gln Val Phe Pro Leu Ile Glu Leu Ser Ala
 530 535 540
 Gln Gly Thr Met Thr Thr Thr Asp Ile Pro Asp Thr Pro Ile Leu Asn
 545 550 555 560
 Thr Thr Asn His Tyr Gly Tyr Gln Gly Thr Gly Ile Ile Val Trp Val
 565 570 575
 Asp Asp Ala Thr Ala Lys Thr Lys Asn Ala Thr Leu Thr Trp Thr Lys
 580 585 590
 Thr Gly Tyr Lys Pro Asn Pro Glu Arg Gln Gly Pro Leu Val Pro Asn
 595 600 605
 Ser Leu Trp Gly Ser Phe Val Asp Val Arg Ser Ile Gln Ser Leu Met
 610 615 620
 Asp Arg Ser Thr Ser Ser Leu Ser Ser Ser Thr Asn Leu Trp Val Ser
 625 630 635 640
 Gly Ile Ala Asp Phe Leu His Glu Asp Gln Lys Gly Asn Gln Arg Ser
 645 650 655
 Tyr Arg His Ser Ser Ala Gly Tyr Ala Leu Gly Gly Gly Phe Phe Thr
 660 665 670
 Ala Ser Glu Asn Phe Phe Asn Phe Ala Phe Cys Gln Leu Phe Gly Tyr
 675 680 685

Asp Lys Asp His Leu Val Ala Lys Asn His Thr His Val Tyr Ala Gly
 690 695 700
 Ala Met Ser Tyr Arg His Leu Gly Glu Ser Lys Thr Leu Ala Lys Ile
 705 710 715 720
 Leu Ser Gly Asn Ser Asp Ser Leu Pro Phe Val Phe Asn Ala Arg Phe
 725 730 735
 Ala Tyr Gly His Thr Asp Asn Asn Met Thr Thr Lys Tyr Thr Gly Tyr
 740 745 750
 Ser Pro Val Lys Gly Ser Trp Gly Asn Asp Ala Phe Gly Ile Glu Cys
 755 760 765
 Gly Gly Ala Ile Pro Val Val Ala Ser Gly Arg Arg Ser Trp Val Asp
 770 775 780
 Thr His Thr Pro Phe Leu Asn Leu Glu Met Ile Tyr Ala His Gln Asn
 785 790 795 800
 Asp Phe Lys Glu Asn Gly Thr Glu Gly Arg Ser Phe Gln Ser Glu Asp
 805 810 815
 Leu Phe Asn Leu Ala Val Pro Val Gly Ile Lys Phe Glu Lys Phe Ser
 820 825 830
 Asp Lys Ser Thr Tyr Asp Leu Ser Ile Ala Tyr Val Pro Asp Val Ile
 835 840 845
 Arg Asn Asp Pro Gly Cys Thr Thr Thr Leu Met Val Ser Gly Asp Ser
 850 855 860
 Trp Ser Thr Cys Gly Thr Ser Leu Ser Arg Gln Ala Leu Leu Val Arg
 865 870 875 880
 Ala Gly Asn His His Ala Phe Ala Ser Asn Phe Glu Val Phe Ser Gln
 885 890 895
 Phe Glu Val Glu Leu Arg Gly Ser Ser Arg Ser Tyr Ala Ile Asp Leu
 900 905 910
 Gly Gly Arg Phe Gly Phe
 915

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATGAAATCCT CTCTTCATTG GTTTGTAATC TCGTCATCTT TAGCACTTCC CTTGTCACTA

AATTTCTCTG	CGTTTGCTGC	TGTTGTTGAA	ATCAATCTAG	GACCTACCAA	TAGCTTCTCT	120
GGACCAGGAA	CCTACACTCC	TCCAGCCCAA	ACAACAAATG	CAGATGGAAC	TATCTATAAT	180
CTAACAGGGG	ATGTCTCAAT	CACCAATGCA	GGATCTCCGA	CAGCTCTAAC	CGCTTCCTGC	240
TTTAAAGAAA	CTACTGGGAA	TCTTTCTTTT	CAAGGCCACG	GCTACCAATT	TCTCCTACAA	300
AATATCGATG	CGGGAGCGAA	CTGTACCCTT	ACCAATACAG	CTGCAAATAA	GCTTCTCTCC	360
TTTTTCAGGAT	TCTCCTATTT	GTCACTAATA	CAAACCACGA	ATGCTACCAC	AGGAACAGGA	420
GCCATCAAGT	CCACAGGAGC	TTGTTCTATT	CAGTCGAACT	ATAGTTGCTA	CTTTGGCCAA	480
AACTTTTTCTA	ATGACAATGG	AGGCGCCCTC	CAAGGCAGCT	CTATCAGTCT	ATCGCTAAAC	540
CCCAACCTAA	CGTTTGCCAA	AAACAAAGCA	ACGCAAAAAG	GGGGTGCCCT	CTATTCCACG	600
GGAGGGATTA	CAATTAACAA	TACGTTAAAC	TCAGCATCAT	TTTCTGAAAA	TACCGCGGCG	660
AACAATGGCG	GAGCCATTTA	CACGGAAGCT	AGCAGTTTTA	TTAGCAGCAA	CAAAGCAATT	720
AGCTTTATAA	ACAATAGTGT	GACCGCAACC	TCAGCTACAG	GGGGAGCCAT	TTACTGTAGT	780
AGTACATCAG	CCCCCAAACC	AGTCTTAACT	CTATCAGACA	ACGGGGAAC	GAACTTTATA	840
GGAAATACAG	CAATTACTAG	TGGTGGGGCG	ATTTATACTG	ACAATCTAGT	TCTTTCTTCT	900
GGAGGACCTA	CGCTTTTTTAA	AAACAACCTCT	GCTATAGATA	CTGCAGCTCC	CTTAGGAGGA	960
GCAATTGCGA	TTGCTGACTC	TGGATCTTTG	AGTCTTTCGG	CTCTTGGTGG	AGACATCACT	1020
TTTGAAGGAA	ACACAGTAGT	CAAAGGAGCT	TCTTCGAGTC	AGACCACTAC	CAGAAATCT	1080
ATTAACATCG	GAAACACCAA	TGCTAAGATT	GTACAGCTGC	GAGCCTCTCA	AGGCAATACT	1140
ATCTACTTCT	ATGATCCTAT	AACAACCTAAC	CATACTGCAG	CTCTCTCAGA	TGCTCTAAAC	1200
TTAAATGGTC	CTGACCTTGC	AGGGAATCCT	GCATATCAAG	GAACCATCGT	ATTTTCTGGA	1260
GAGAAGCTCT	CGGAAGCAGA	AGCTGCAGAA	GCTGATAATC	TCAAATCTAC	AATTCAGCAA	1320
CCTCTAACTC	TTGCGGGAGG	GCAACTCTCT	CTTAAATCAG	GAGTCACTCT	AGTTGCTAAG	1380
TCCTTTTTCGC	AATCTCCGGG	CTCTACCCTC	CTCATGGATG	CAGGGACCAC	ATTAGAAACC	1440
GCTGATGGGA	TCACTATCAA	TAATCTTGTT	CTCAATGTAG	ATTCTCTAAA	AGAGACCAAG	1500
AAGGCTACGC	TAAAAGCAAC	ACAAGCAAGT	CAGACAGTCA	CTTTATCTGG	ATCGCTCTCT	1560
CTTGTAGTCA	CTTCTGGAAA	TGTCTACGAA	GATGTCTCTT	GGAATAACCC	TCAAGTCTTT	1620
TCTTGCTCTCA	CTCTTACTGC	TGACGACCCC	GCGAATATTC	ACATCACAGA	CTTAGCTGCT	1680
GATCCCCTAG	AAAAAAATCC	TATCCATTGG	GGATACCAAG	GGAATTGGGC	ATTATCTTGG	1740
CAAGAGGATA	CTGCGACTAA	ATCCAAAGCA	GCGACTCTTA	CCTGGACAAA	AACAGGATAC	1800
AATCCGAATC	CTGAGCGTCG	TGGAACCTTA	GTTGCTAACA	CGCTATGGGG	ATCCTTTGTT	1860
GATGTGCGCT	CCATACAACA	GCTTGTAGCC	ACTAAAGTAC	GCCAATCTCA	AGAAACTCGC	1920
GGCATCTGGT	GTGAAGGGAT	CTCGAACTTC	TTCCATAAAG	ATAGCACGAA	GATAAATAAA	1980
GGTTTTTCGCC	ACATAAGTGC	AGGTTATGTT	GTAGGAGCGA	CTACAACATT	AGCTTCTGAT	2040
AATCTTATCA	CTGCAGCCTT	CTGCCAATTA	TTCCGGGAAAG	ATAGAGATCA	CTTTATAAAT	2100
AAAAATAGAG	CTTCTGCCTA	TGCAGCTTCT	CTCCATCTCC	AGCATCTAGC	GACCTTGTCT	2160
TCTCCAAGCT	TGTTACGCTA	CCTTCCTGGA	TCTGAAAGTG	AGCAGCCTGT	CCTCTTTGAT	2220
GCTCAGATCA	GCTATATCTA	TAGTAAAAAT	ACTATGAAAA	CCTATTACAC	CCAAGCACCA	2280
AAGGGAGAGA	GCTCGTGGTA	TAATGACGGT	TGCGCTCTGG	AACTTGCGAG	CTCCCTACCA	2340
CACACTGCTT	TAAGCCATGA	GGGTCTCTTC	CACGCGTATT	TTCTTTTCAT	CAAAGTAGAA	2400
GCTTCGTACA	TACACCAAGA	TAGCTTCAAA	GAACGTAATA	CTACCTTGGT	ACGATCTTTC	2460
GATAGCGGTG	ATTTAATTAA	CGTCTCTGTG	CCTATTGGAA	TTACCTTCGA	GAGATTCTCG	2520
AGAAACGAGC	GTGCGTCTTA	CGAAGCTACT	GTCATCTACG	TTGCCGATGT	CTATCGTAAG	2580
AATCCTGACT	GCACGACAGC	TCTCCTAATC	AACAATACCT	CGTGGAAGAA	TACAGGAACG	2640
AATCTCTCAA	GACAAGCTGG	TATCGGAAGA	GCAGGGATCT	TTTATGCCTT	CTCTCCAAAT	2700
CTTGAGGTCA	CAAGTAACCT	ATCTATGGAA	ATTCGTGGAT	CTTCACGCAG	CTACAATGCA	2760
GATCTTGGAG	GTAAGTTCCA	GTTCTAA				2787

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Lys	Ser	Ser	Leu	His	Trp	Phe	Val	Ile	Ser	Ser	Ser	Leu	Ala	Leu	1	5	10	15
Pro	Leu	Ser	Leu	Asn	Phe	Ser	Ala	Phe	Ala	Ala	Val	Val	Glu	Ile	Asn	20	25	30	
Leu	Gly	Pro	Thr	Asn	Ser	Phe	Ser	Gly	Pro	Gly	Thr	Tyr	Thr	Pro	Pro	35	40	45	
Ala	Gln	Thr	Thr	Asn	Ala	Asp	Gly	Thr	Ile	Tyr	Asn	Leu	Thr	Gly	Asp	50	55	60	
Val	Ser	Ile	Thr	Asn	Ala	Gly	Ser	Pro	Thr	Ala	Leu	Thr	Ala	Ser	Cys	65	70	75	80
Phe	Lys	Glu	Thr	Thr	Gly	Asn	Leu	Ser	Phe	Gln	Gly	His	Gly	Tyr	Gln	85	90	95	
Phe	Leu	Leu	Gln	Asn	Ile	Asp	Ala	Gly	Ala	Asn	Cys	Thr	Phe	Thr	Asn	100	105	110	
Thr	Ala	Ala	Asn	Lys	Leu	Leu	Ser	Phe	Ser	Gly	Phe	Ser	Tyr	Leu	Ser	115	120	125	
Leu	Ile	Gln	Thr	Thr	Asn	Ala	Thr	Thr	Gly	Thr	Gly	Ala	Ile	Lys	Ser	130	135	140	
Thr	Gly	Ala	Cys	Ser	Ile	Gln	Ser	Asn	Tyr	Ser	Cys	Tyr	Phe	Gly	Gln	145	150	155	160
Asn	Phe	Ser	Asn	Asp	Asn	Gly	Gly	Ala	Leu	Gln	Gly	Ser	Ser	Ile	Ser	165	170	175	
Leu	Ser	Leu	Asn	Pro	Asn	Leu	Thr	Phe	Ala	Lys	Asn	Lys	Ala	Thr	Gln	180	185	190	
Lys	Gly	Gly	Ala	Leu	Tyr	Ser	Thr	Gly	Gly	Ile	Thr	Ile	Asn	Asn	Thr	195	200	205	
Leu	Asn	Ser	Ala	Ser	Phe	Ser	Glu	Asn	Thr	Ala	Ala	Asn	Asn	Gly	Gly	210	215	220	
Ala	Ile	Tyr	Thr	Glu	Ala	Ser	Ser	Phe	Ile	Ser	Ser	Asn	Lys	Ala	Ile	225	230	235	240
Ser	Phe	Ile	Asn	Asn	Ser	Val	Thr	Ala	Thr	Ser	Ala	Thr	Gly	Gly	Ala	245	250	255	
Ile	Tyr	Cys	Ser	Ser	Thr	Ser	Ala	Pro	Lys	Pro	Val	Leu	Thr	Leu	Ser	260	265	270	
Asp	Asn	Gly	Glu	Leu	Asn	Phe	Ile	Gly	Asn	Thr	Ala	Ile	Thr	Ser	Gly	275	280	285	
Gly	Ala	Ile	Tyr	Thr	Asp	Asn	Leu	Val	Leu	Ser	Ser	Gly	Gly	Pro	Thr	290	295	300	

Leu Phe Lys Asn Asn Ser Ala Ile Asp Thr Ala Ala Pro Leu Gly Gly
 305 310 315 320
 Ala Ile Ala Ile Ala Asp Ser Gly Ser Leu Ser Leu Ser Ala Leu Gly
 325 330 335
 Gly Asp Ile Thr Phe Glu Gly Asn Thr Val Val Lys Gly Ala Ser Ser
 340 345 350
 Ser Gln Thr Thr Thr Arg Asn Ser Ile Asn Ile Gly Asn Thr Asn Ala
 355 360 365
 Lys Ile Val Gln Leu Arg Ala Ser Gln Gly Asn Thr Ile Tyr Phe Tyr
 370 375 380
 Asp Pro Ile Thr Thr Asn His Thr Ala Ala Leu Ser Asp Ala Leu Asn
 385 390 395 400
 Leu Asn Gly Pro Asp Leu Ala Gly Asn Pro Ala Tyr Gln Gly Thr Ile
 405 410 415
 Val Phe Ser Gly Glu Lys Leu Ser Glu Ala Glu Ala Ala Glu Ala Asp
 420 425 430
 Asn Leu Lys Ser Thr Ile Gln Gln Pro Leu Thr Leu Ala Gly Gly Gln
 435 440 445
 Leu Ser Leu Lys Ser Gly Val Thr Leu Val Ala Lys Ser Phe Ser Gln
 450 455 460
 Ser Pro Gly Ser Thr Leu Leu Met Asp Ala Gly Thr Thr Leu Glu Thr
 465 470 475 480
 Ala Asp Gly Ile Thr Ile Asn Asn Leu Val Leu Asn Val Asp Ser Leu
 485 490 495
 Lys Glu Thr Lys Lys Ala Thr Leu Lys Ala Thr Gln Ala Ser Gln Thr
 500 505 510
 Val Thr Leu Ser Gly Ser Leu Ser Leu Val Asp Pro Ser Gly Asn Val
 515 520 525
 Tyr Glu Asp Val Ser Trp Asn Asn Pro Gln Val Phe Ser Cys Leu Thr
 530 535 540
 Leu Thr Ala Asp Asp Pro Ala Asn Ile His Ile Thr Asp Leu Ala Ala
 545 550 555 560
 Asp Pro Leu Glu Lys Asn Pro Ile His Trp Gly Tyr Gln Gly Asn Trp
 565 570 575
 Ala Leu Ser Trp Gln Glu Asp Thr Ala Thr Lys Ser Lys Ala Ala Thr
 580 585 590
 Leu Thr Trp Thr Lys Thr Gly Tyr Asn Pro Asn Pro Glu Arg Arg Gly
 595 600 605

Thr	Leu	Val	Ala	Asn	Thr	Leu	Trp	Gly	Ser	Phe	Val	Asp	Val	Arg	Ser		
610						615					620						
Ile	Gln	Gln	Leu	Val	Ala	Thr	Lys	Val	Arg	Gln	Ser	Gln	Glu	Thr	Arg		
625					630					635					640		
Gly	Ile	Trp	Cys	Glu	Gly	Ile	Ser	Asn	Phe	Phe	His	Lys	Asp	Ser	Thr		
				645					650					655			
Lys	Ile	Asn	Lys	Gly	Phe	Arg	His	Ile	Ser	Ala	Gly	Tyr	Val	Val	Gly		
		660						665					670				
Ala	Thr	Thr	Thr	Leu	Ala	Ser	Asp	Asn	Leu	Ile	Thr	Ala	Ala	Phe	Cys		
		675					680					685					
Gln	Leu	Phe	Gly	Lys	Asp	Arg	Asp	His	Phe	Ile	Asn	Lys	Asn	Arg	Ala		
	690					695					700						
Ser	Ala	Tyr	Ala	Ala	Ser	Leu	His	Leu	Gln	His	Leu	Ala	Thr	Leu	Ser		
705					710					715					720		
Ser	Pro	Ser	Leu	Leu	Arg	Tyr	Leu	Pro	Gly	Ser	Glu	Ser	Glu	Gln	Pro		
			725						730					735			
Val	Leu	Phe	Asp	Ala	Gln	Ile	Ser	Tyr	Ile	Tyr	Ser	Lys	Asn	Thr	Met		
			740					745					750				
Lys	Thr	Tyr	Tyr	Thr	Gln	Ala	Pro	Lys	Gly	Glu	Ser	Ser	Trp	Tyr	Asn		
		755					760					765					
Asp	Gly	Cys	Ala	Leu	Glu	Leu	Ala	Ser	Ser	Leu	Pro	His	Thr	Ala	Leu		
	770					775					780						
Ser	His	Glu	Gly	Leu	Phe	His	Ala	Tyr	Phe	Pro	Phe	Ile	Lys	Val	Glu		
785					790					795					800		
Ala	Ser	Tyr	Ile	His	Gln	Asp	Ser	Phe	Lys	Glu	Arg	Asn	Thr	Thr	Leu		
				805					810						815		
Val	Arg	Ser	Phe	Asp	Ser	Gly	Asp	Leu	Ile	Asn	Val	Ser	Val	Pro	Ile		
			820					825					830				
Gly	Ile	Thr	Phe	Glu	Arg	Phe	Ser	Arg	Asn	Glu	Arg	Ala	Ser	Tyr	Glu		
		835					840					845					
Ala	Thr	Val	Ile	Tyr	Val	Ala	Asp	Val	Tyr	Arg	Lys	Asn	Pro	Asp	Cys		
						855					860						
Thr	Thr	Ala	Leu	Leu	Ile	Asn	Asn	Thr	Ser	Trp	Lys	Thr	Thr	Gly	Thr		
865					870					875					880		
Asn	Leu	Ser	Arg	Gln	Ala	Gly	Ile	Gly	Arg	Ala	Gly	Ile	Phe	Tyr	Ala		
				885				890						895			
Phe	Ser	Pro	Asn	Leu	Glu	Val	Thr	Ser	Asn	Leu	Ser	Met	Glu	Ile	Arg		
			900					905					910				
Gly	Ser	Ser	Arg	Ser	Tyr	Asn	Ala	Asp	Leu	Gly	Gly	Lys	Phe	Gln	Phe		
		915					920					925					

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2793 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATGAAAATAC	CCTTGCACAA	ACTCCTGATC	TCTTCGACTC	TTGTCACTCC	CATTCTATTG	60
AGCATTGCAA	CTTACGGAGC	AGATGCTTCT	TTATCCCCTA	CAGATAGCTT	TGATGGAGCG	120
GGCGGCTCTA	CATTTACTCC	AAAATCTACA	GCAGATGCCA	ATGGAACGAA	CTATGTCTTA	180
TCAGGAAATG	TCTATATAAA	CGATGCTGGG	AAAGGCACAG	CATTAACAGG	CTGCTGCTTT	240
ACAGAAACTA	CGGGTGATCT	GACATTTACT	GGAAAGGGAT	ACTCATTTTC	ATTC AACACG	300
G TAGATGCGG	GTTCGAATGC	AGGAGCTGCG	GCAAGCACAA	CTGCTGATAA	AGCCCTAACA	360
TTCACAGGAT	TTTCTAACCT	TTCCTTCATT	GCAGCTCCTG	GA ACTACAGT	TGCTTCAGGA	420
AAAAGTACTT	TAAGTTCTGC	AGGAGCCTTA	AATCTTACCG	ATAATGGAAC	GATTCTCTTT	480
AGCCAAAACG	TCTCCAATGA	AGCTAATAAC	AATGGCGGAG	CGATCACCAC	AAAAACTCTT	540
TCTATTTCTG	GGAATACCTC	TTCTATAACC	TTC ACTAGTA	ATAGCGCAAA	AAAAATTAGGT	600
GGAGCGATCT	ATAGCTCTGC	GGCTGCAAGT	ATTT CAGGAA	ACACCGGCCA	GTTAGTCTTT	660
ATGAATAATA	AAGGAGAAAC	TGGGGGCGGG	GCTCTGGGCT	TTGAAGCCAG	CTCCTCGATT	720
ACTCAAATA	GCTCCCTTTT	CTTCTCTGGA	AACACTGCAA	CAGATGCTGC	AGGCAAGGGC	780
GGGGCCATTT	ATTGTGAAAA	AACAGGAGAG	ACTCCTACTC	TTACTATCTC	TGGAATAATA	840
AGTCTGACCT	TCGCCGAGAA	CTCTTCAGTA	ACTCAAGGCG	GAGCAATCTG	TGCCCATGGT	900
CTAGATCTTT	CCGCTGCTGG	CCCTACCCTA	TTTTCAAATA	ATAGATGCGG	GAACACAGCT	960
GCAGGCAAGG	GCGGCCTAT	TGCAATTGCC	GACTCTGGAT	CTTTAAGTCT	CTCTGCAAAT	1020
CAAGGAGACA	TCACGTT CCT	TGGCAACACT	CTAACCTCAA	CCTCCGCGCC	AACATCGACA	1080
CGGAATGCTA	TCTACCTGGG	ATCGTCAGCA	AAAATTACGA	ACTTAAGGGC	AGCCCAAGGC	1140
CAATCTATCT	ATTTCTATGA	TCCGATTGCA	TCTAACACCA	CAGGAGCTTC	AGACGTTCTG	1200
ACCATCAACC	AACCGGATAG	CAACTCGCCT	TTAGATTATT	CAGGAACGAT	TGTATTTTCT	1260
GGGGAAAAGC	TCTCTGCAGA	TGAAGCGAAA	GCTGCTGATA	ACTTCACATC	TATATTAAAG	1320
CAACCATTGG	CTCTAGCCTC	TGGAACCTTA	GCACTCAAAG	GAAATGTCGA	GTTAGATGTC	1380
AATGGTTTCA	CACAGACTGA	AGGCTCTACA	CTCCTCATGC	AACCAGGAAC	AAAGCTCAAA	1440
GCAGATACTG	AAGCTATCAG	TCTTACCAAA	CTTGTCGTTG	ATCTTTCTGC	CTTAGAGGGA	1500
AATAAGAGTG	TGTCCATTGA	AACAGCAGGA	GCCAACAAAA	CTATAACTCT	AACCTCTCCT	1560
CTTGTTTTCC	AAGATAGTAG	CGGCAATTTT	TATGAAAGCC	ATACGATAAA	CCAAGCCTTC	1620
ACGCAGCCTT	TGGTGGTATT	CACTGCTGCT	ACTGCTGCTA	GCGATATTTA	TATCGATGCG	1680
CTTCTCACTT	CTCCAGTACA	AACTCCAGAA	CCTCATTACG	GGTATCAGGG	ACATTGGGAA	1740
GCCACTTGGG	CAGACACATC	AACTGCAAAA	TCAGGA ACTA	TGACTTGGGT	AACTACGGGC	1800
TACAACCCTA	ATCCTGAGCG	TAGAGCTTCC	G TAGTTCCCG	ATT CATTATG	GGCATCCTTT	1860
ACTGACATTC	GCACTCTACA	GCAGATCATG	ACATCTCAAG	CGAATAGTAT	CTATCAGCAA	1920
CGAGGACTCT	GGGCATCAGG	AACTGCGAAT	TTCTTCCATA	AGGATAAATC	AGGAACTAAC	1980
CAAGCATTCC	GACATAAAAG	CTACGGCTAT	ATTGTTGGAG	GAAGTGCTGA	AGATTTTCT	2040
GAAAATATCT	TCAGTG TAGC	TTTCTGCCAG	CTCTTCGGTA	AAGATAAAGA	CCTGTTTATA	2100
GTTGAAAATA	CCTCTCATAA	CTATTTAGCG	TCGCTATACC	TGCAACATCG	AGCATTCCTA	2160
GGAGGACTTC	CCATGCCCTC	ATTTGGAAGT	ATCACC GACA	TGCTGAAAGA	TATTCCTCTC	2220
ATTTTGAATG	CCCAGCTAAG	CTACAGCTAC	ACTAAAAATG	ATATGGATAC	TCGCTATACT	2280
TCTTATCCTG	AAGTCAAGG	TTCTTG GACC	AATAATTCTG	GGGCTCTAGA	GCTCGGAGGA	2340
TCTCTGGCTC	TATATCTCCC	TAAAGAAGCA	CCGTTCTTCC	AGGGATATTT	CCCCTTCTTA	2400
AAGTTCCAGG	CAGTCTACAG	CCGCCAACAA	AACTTTAAAG	AGAGTGGCGC	TGAAGCCCGT	2460
GCTTTTGTATG	ATGGAGACCT	AGTGA ACTGC	TCTATCCCTG	TCGGCATT CG	GTTAGAAAAA	2520
ATCTCCGAAG	ATGAAAAAAA	TAATTT CGAG	ATTTCTCTAG	CCAACATTGG	TGATGTGTAT	2580
CGTAAAAATC	CCCGTT CGCG	TACTTCTCTA	ATGGTCAGTG	GAGCCTCTTG	GACTTCGCTA	2640
TGTAAAAACC	TCGCACGACA	AGCCTTCTTA	GCAAGTGCTG	GAAGCCATCT	GACTCTCTCC	2700

2760
2793

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met 1	Lys	Ile	Pro	Leu 5	His	Lys	Leu	Leu	Ile 10	Ser	Ser	Thr	Leu	Val 15	Thr
Pro	Ile	Leu	Leu 20	Ser	Ile	Ala	Thr	Tyr 25	Gly	Ala	Asp	Ala	Ser 30	Leu	Ser
Pro	Thr	Asp 35	Ser	Phe	Asp	Gly	Ala 40	Gly	Gly	Ser	Thr	Phe 45	Thr	Pro	Lys
Ser	Thr 50	Ala	Asp	Ala	Asn	Gly 55	Thr	Asn	Tyr	Val	Leu 60	Ser	Gly	Asn	Val
Tyr 65	Ile	Asn	Asp	Ala	Gly 70	Lys	Gly	Thr	Ala	Leu 75	Thr	Gly	Cys	Cys	Phe 80
Thr	Glu	Thr	Thr	Gly 85	Asp	Leu	Thr	Phe	Thr 90	Gly	Lys	Gly	Tyr	Ser 95	Phe
Ser	Phe	Asn	Thr 100	Val	Asp	Ala	Gly	Ser 105	Asn	Ala	Gly	Ala	Ala 110	Ala	Ser
Thr	Thr	Ala 115	Asp	Lys	Ala	Leu	Thr 120	Phe	Thr	Gly	Phe	Ser 125	Asn	Leu	Ser
Phe 130	Ile	Ala	Ala	Pro	Gly 135	Thr	Thr	Val	Ala	Ser	Gly 140	Lys	Ser	Thr	Leu
Ser 145	Ser	Ala	Gly	Ala	Leu 150	Asn	Leu	Thr	Asp	Asn 155	Gly	Thr	Ile	Leu	Phe 160
Ser	Gln	Asn	Val	Ser 165	Asn	Glu	Ala	Asn	Asn 170	Asn	Gly	Gly	Ala	Ile 175	Thr
Thr	Lys	Thr 180	Leu	Ser	Ile	Ser	Gly 185	Asn	Thr	Ser	Ser	Ile 190	Thr	Phe	Thr
Ser	Asn	Ser 195	Ala	Lys	Lys	Leu	Gly 200	Gly	Ala	Ile	Tyr	Ser 205	Ser	Ala	Ala
Ala 210	Ser	Ile	Ser	Gly	Asn	Thr 215	Gly	Gln	Leu	Val	Phe 220	Met	Asn	Asn	Lys
Gly 225	Glu	Thr	Gly	Gly 230	Gly	Ala	Leu	Gly	Phe	Glu 235	Ala	Ser	Ser	Ser	Ile 240

Thr Gln Asn Ser Ser Leu Phe Phe Ser Gly Asn Thr Ala Thr Asp Ala
 245 250 255
 Ala Gly Lys Gly Gly Ala Ile Tyr Cys Glu Lys Thr Gly Glu Thr Pro
 260 265 270
 Thr Leu Thr Ile Ser Gly Asn Lys Ser Leu Thr Phe Ala Glu Asn Ser
 275 280 285
 Ser Val Thr Gln Gly Gly Ala Ile Cys Ala His Gly Leu Asp Leu Ser
 290 295 300
 Ala Ala Gly Pro Thr Leu Phe Ser Asn Asn Arg Cys Gly Asn Thr Ala
 305 310 315 320
 Ala Gly Lys Gly Gly Ala Ile Ala Ile Ala Asp Ser Gly Ser Leu Ser
 325 330 335
 Leu Ser Ala Asn Gln Gly Asp Ile Thr Phe Leu Gly Asn Thr Leu Thr
 340 345 350
 Ser Thr Ser Ala Pro Thr Ser Thr Arg Asn Ala Ile Tyr Leu Gly Ser
 355 360 365
 Ser Ala Lys Ile Thr Asn Leu Arg Ala Ala Gln Gly Gln Ser Ile Tyr
 370 375 380
 Phe Tyr Asp Pro Ile Ala Ser Asn Thr Thr Gly Ala Ser Asp Val Leu
 385 390 395 400
 Thr Ile Asn Gln Pro Asp Ser Asn Ser Pro Leu Asp Tyr Ser Gly Thr
 405 410 415
 Ile Val Phe Ser Gly Glu Lys Leu Ser Ala Asp Glu Ala Lys Ala Ala
 420 425 430
 Asp Asn Phe Thr Ser Ile Leu Lys Gln Pro Leu Ala Leu Ala Ser Gly
 435 440 445
 Thr Leu Ala Leu Lys Gly Asn Val Glu Leu Asp Val Asn Gly Phe Thr
 450 455 460
 Gln Thr Glu Gly Ser Thr Leu Leu Met Gln Pro Gly Thr Lys Leu Lys
 465 470 475 480
 Ala Asp Thr Glu Ala Ile Ser Leu Thr Lys Leu Val Val Asp Leu Ser
 485 490 495
 Ala Leu Glu Gly Asn Lys Ser Val Ser Ile Glu Thr Ala Gly Ala Asn
 500 505 510
 Lys Thr Ile Thr Leu Thr Ser Pro Leu Val Phe Gln Asp Ser Ser Gly
 515 520 525
 Asn Phe Tyr Glu Ser His Thr Ile Asn Gln Ala Phe Thr Gln Pro Leu
 530 535 540

Val	Val	Phe	Thr	Ala	Ala	Thr	Ala	Ala	Ser	Asp	Ile	Tyr	Ile	Asp	Ala	545	550	555	560
Leu	Leu	Thr	Ser	Pro	Val	Gln	Thr	Pro	Glu	Pro	His	Tyr	Gly	Tyr	Gln	565	570		575
Gly	His	Trp	Glu	Ala	Thr	Trp	Ala	Asp	Thr	Ser	Thr	Ala	Lys	Ser	Gly	580	585		590
Thr	Met	Thr	Trp	Val	Thr	Thr	Gly	Tyr	Asn	Pro	Asn	Pro	Glu	Arg	Arg	595	600		605
Ala	Ser	Val	Val	Pro	Asp	Ser	Leu	Trp	Ala	Ser	Phe	Thr	Asp	Ile	Arg	610	615		620
Thr	Leu	Gln	Gln	Ile	Met	Thr	Ser	Gln	Ala	Asn	Ser	Ile	Tyr	Gln	Gln	625	630	635	640
Arg	Gly	Leu	Trp	Ala	Ser	Gly	Thr	Ala	Asn	Phe	Phe	His	Lys	Asp	Lys	645	650		655
Ser	Gly	Thr	Asn	Gln	Ala	Phe	Arg	His	Lys	Ser	Tyr	Gly	Tyr	Ile	Val	660	665		670
Gly	Gly	Ser	Ala	Glu	Asp	Phe	Ser	Glu	Asn	Ile	Phe	Ser	Val	Ala	Phe	675	680	685	
Cys	Gln	Leu	Phe	Gly	Lys	Asp	Lys	Asp	Leu	Phe	Ile	Val	Glu	Asn	Thr	690	695	700	
Ser	His	Asn	Tyr	Leu	Ala	Ser	Leu	Tyr	Leu	Gln	His	Arg	Ala	Phe	Leu	705	710	715	720
Gly	Gly	Leu	Pro	Met	Pro	Ser	Phe	Gly	Ser	Ile	Thr	Asp	Met	Leu	Lys	725	730		735
Asp	Ile	Pro	Leu	Ile	Leu	Asn	Ala	Gln	Leu	Ser	Tyr	Ser	Tyr	Thr	Lys	740	745		750
Asn	Asp	Met	Asp	Thr	Arg	Tyr	Thr	Ser	Tyr	Pro	Glu	Ala	Gln	Gly	Ser	755	760	765	
Trp	Thr	Asn	Asn	Ser	Gly	Ala	Leu	Glu	Leu	Gly	Gly	Ser	Leu	Ala	Leu	770	775	780	
Tyr	Leu	Pro	Lys	Glu	Ala	Pro	Phe	Phe	Gln	Gly	Tyr	Phe	Pro	Phe	Leu	785	790	795	800
Lys	Phe	Gln	Ala	Val	Tyr	Ser	Arg	Gln	Gln	Asn	Phe	Lys	Glu	Ser	Gly	805	810		815
Ala	Glu	Ala	Arg	Ala	Phe	Asp	Asp	Gly	Asp	Leu	Val	Asn	Cys	Ser	Ile	820	825		830
Pro	Val	Gly	Ile	Arg	Leu	Glu	Lys	Ile	Ser	Glu	Asp	Glu	Lys	Asn	Asn	835	840	845	

Phe Glu Ile Ser Leu Ala Asn Ile Gly Asp Val Tyr Arg Lys Asn Pro
 850 855 860
 Arg Ser Arg Thr Ser Leu Met Val Ser Gly Ala Ser Trp Thr Ser Leu
 865 870 875 880
 Cys Lys Asn Leu Ala Arg Gln Ala Phe Leu Ala Ser Ala Gly Ser His
 885 890 895
 Leu Thr Leu Ser Pro His Val Glu Leu Ser Gly Glu Ala Ala Tyr Glu
 900 905 910
 Leu Arg Gly Ser Ala His Ile Tyr Asn Val Asp Cys Gly Leu Arg Tyr
 915 920 925
 Ser Phe
 930

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAAGACAATA	TAAGGTACCG	TCATAACAGC	GGGGGTTATG	CACTAGGGAT	CACAGCAACA	60
ACTCCTGCCG	AGGATCAGCT	TACTTTTGCC	TTCTGCCAGC	TCTTTGCTAG	AGATCGCAAT	120
CATATTACAG	GTAAGAACCA	CGGAGATACT	TACGGTGCCT	CTTTGTATTT	CCACCATACA	180
GAAGGGCTCT	TCGACATCGC	CAATTTCCCTC	TGGGGAAAAG	CAACCCGAGC	TCCCTGGGTG	240
CTCTCTGAGA	TCTCCCAGAT	CATTCCTTTA	TCGTTTCGATG	CTAAATTCAG	TTATCTCCAT	300
ACAGACAACC	ACATGAAGAC	ATATTATACC	GATAACTCTA	TCATCAAGGG	TTCTTGGAGA	360
AACGATGCCT	TCTGTGCAGA	TCTTGGAGCT	AGCCTGCCTT	TTGTTATTTT	CGTTCCTGAT	420
CTTCTGAAAG	AAGTCGAACC	TTTTGTCAAA	GTACAGTATA	TCTATGCGCA	TCAGCAAGAC	480
TTCTACGAGC	GTCATGCTGA	AGGACGCGCT	TTCAATAAAA	GCGAGCTTAT	CAACGTAGAG	540
ATTCTTATAG	GCGTCACCTT	CGAAAGAGAC	TCAAATCAG	AAAAGGGAAC	TTACGATCTT	600
ACTCTTATGT	ATATACTCGA	TGCTTACCGA	CGCAATCCTA	AATGTCAAAC	TTCCCTAATA	660
GCTAGCGATG	CTAACTGGAT	GGCCTATGGT	ACCAACCTCG	CACGACAAGG	TTTTTCTGTT	720
CGTGCTGCCA	ACCATTTCCTA	AGTGAACCCC	CACATGGAAA	TCTTCGGTCA	ATTCGCTTTT	780
GAAGTACGAA	GTTCTTCACG	AAATTATAAT	ACAAACCTAG	GCTCTAAGTT	TTGTTTCTAG	840

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Glu 1	Asp	Asn	Ile	Arg 5	Tyr	Arg	His	Asn	Ser 10	Gly	Gly	Tyr	Ala	Leu 15	Gly
Ile	Thr	Ala	Thr 20	Thr	Pro	Ala	Glu	Asp 25	Gln	Leu	Thr	Phe	Ala 30	Phe	Cys
Gln	Leu	Phe 35	Ala	Arg	Asp	Arg	Asn 40	His	Ile	Thr	Gly	Lys 45	Asn	His	Gly
Asp	Thr 50	Tyr	Gly	Ala	Ser	Leu 55	Tyr	Phe	His	His	Thr 60	Glu	Gly	Leu	Phe
Asp 65	Ile	Ala	Asn	Phe	Leu 70	Trp	Gly	Lys	Ala	Thr 75	Arg	Ala	Pro	Trp	Val 80
Leu	Ser	Glu	Ile	Ser 85	Gln	Ile	Ile	Pro	Leu 90	Ser	Phe	Asp	Ala	Lys 95	Phe
Ser	Tyr	Leu	His 100	Thr	Asp	Asn	His	Met 105	Lys	Thr	Tyr	Tyr	Thr 110	Asp	Asn
Ser	Ile	Ile 115	Lys	Gly	Ser	Trp	Arg 120	Asn	Asp	Ala	Phe	Cys 125	Ala	Asp	Leu
Gly	Ala	Ser	Leu	Pro	Phe	Val 135	Ile	Ser	Val	Pro	Tyr 140	Leu	Leu	Lys	Glu
Val 145	Glu	Pro	Phe	Val	Lys 150	Val	Gln	Tyr	Ile 155	Tyr	Ala	His	Gln	Gln	Asp 160
Phe	Tyr	Glu	Arg	His 165	Ala	Glu	Gly	Arg	Ala 170	Phe	Asn	Lys	Ser	Glu 175	Leu
Ile	Asn	Val	Glu 180	Ile	Pro	Ile	Gly	Val 185	Thr	Phe	Glu	Arg	Asp 190	Ser	Lys
Ser	Glu	Lys 195	Gly	Thr	Tyr	Asp	Leu 200	Thr	Leu	Met	Tyr	Ile 205	Leu	Asp	Ala
Tyr	Arg 210	Arg	Asn	Pro	Lys	Cys 215	Gln	Thr	Ser	Leu	Ile 220	Ala	Ser	Asp	Ala
Asn 225	Trp	Met	Ala	Tyr	Gly 230	Thr	Asn	Leu	Ala 235	Arg	Gln	Gly	Phe	Ser	Val 240
Arg	Ala	Ala	Asn	His 245	Phe	Gln	Val	Asn	Pro 250	His	Met	Glu	Ile	Phe 255	Gly
Gln	Phe	Ala	Phe 260	Glu	Val	Arg	Ser	Ser 265	Ser	Arg	Asn	Tyr	Asn 270	Thr	Asn
Leu	Gly 275	Ser	Lys	Phe	Cys	Phe									

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1545 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATGACCATAC	TTCGAAATTT	TCTTACCTGC	TCGGCTTTAT	TCCTCGCTCT	CCCTGCAGCA	60
GCACAAGTTG	TATATCTTCA	TGAAAGTGAT	GGTTATAACG	GTGCTATCAA	TAATAAAAGC	120
TTAGAACCTA	AAATTACCTG	TTATCCAGAA	GGAACCTCTT	ACATCTTTCT	AGATGACGTG	180
AGGATTTCCA	ACGTTAAGCA	TGATCAAGAA	GATGCTGGGG	TTTTTATAAA	TCGATCTGGG	240
AATCTTTTTT	TCATGGGCAA	CCGTTGCAAC	TTCACCTTTC	ACAACCTTAT	GACCGAGGGT	300
TTTGGCGCTG	CCATTTTCGAA	CCGCGTTGGA	GACACCACTC	TCACTCTCTC	TAATTTTTCT	360
TACTTAACGT	TCACCTCAGC	ACCTCTACTA	CCTCAAGGAC	AAGGAGCGAT	TTATAGTCTT	420
GGTTCCGTGA	TGATCGAAAA	TAGTGAGGAA	GTGACTTTCT	GTGGGAACTA	CTCTTCGTGG	480
AGTGGAGCTG	CGATTTATAC	TCCCTACCTT	TTAGGTTCTA	AGGCGAGTCG	TCCTTCAGTA	540
AATCTCAGCG	GGAACCGCTA	CCTGGTGTTT	AGAGACTATG	TGAGCCAAGG	TTATGGCGGC	600
GCCGTATCTA	CCCACAATCT	CACACTCACG	ACTCGAGGAC	CTTCGTGTTT	TGAAAATAAT	660
CATGCTTATC	ATGACGTGAA	TAGTAATGGA	GGAGCCATTG	CCATTGCTCC	TGGAGGATCG	720
ATCTCTATAT	CCGTGAAAAG	CGGAGATCTC	ATCTTCAAAG	GAAATACAGC	ATCACAAGAC	780
GGAAATACAA	TACACAACCTC	CATCCATCTG	CAATCTGGAG	CACAGTTTAA	GAACCTACGT	840
GCTGTTTCAG	AATCCGGAGT	TTATTTCTAT	GATCCTATAA	GCCATAGCGA	GTGCGATAAA	900
ATTACAGATC	TTGTAATCAA	TGCTCCTGAA	GGAAAGGAAA	CTTATGAAGG	AACAATTAGC	960
TTCTCAGGAC	TATGCCTGGA	TGATCATGAA	GTTTGTGCGG	AAAATCTTAC	TTCCACAATC	1020
CTACAAGATG	TCACATTAGC	AGGAGGAACT	CTCTCTCTAT	CGGATGGGGT	TACCTTGCAA	1080
CTGCATTCTT	TTAAGCAGGA	AGCAAGCTCT	ACGCTTACTA	TGTCTCCAGG	AACCACTCTG	1140
CTCTGCTCAG	GAGATGCTCG	GGTTCAGAAT	CTGCACATCC	TGATTGAAGA	TACCGACAAC	1200
TTTGTTCCCTG	TAAGGATTCG	CGCCGAGGAC	AAGGATGCTC	TTGTCTCATT	AGAAAACTT	1260
AAAGTTGCCT	TTGAGGCTTA	TTGGTCCGTC	TATGACTTTC	CTCAATTTAA	GGAAGCCTTT	1320
ACGATTCCCTC	TTCTTGAACCT	TCTAGGGCCT	TCTTTTGACA	GTCTTCTCCT	AGGGGAGACC	1380
ACTTTGGAGA	GAACCCAAGT	CACAACAGAG	AATGACGCCG	TTGAGGTTT	CTGGTCCCTA	1440
AGCTGGGAAG	AGTACCCCCC	TTCTCTGGAT	AAAGACAGAA	GGATCACACC	AACTAAGAAA	1500
ACTGTTTTCC	TCACTTGGA	TCCTGAGATC	ACTTCTACGC	CATAA		1545

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 514 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Thr	Ile	Leu	Arg	Asn	Phe	Leu	Thr	Cys	Ser	Ala	Leu	Phe	Leu	Ala
1					5				10					15	
Leu	Pro	Ala	Ala	Ala	Gln	Val	Val	Tyr	Leu	His	Glu	Ser	Asp	Gly	Tyr
		20						25					30		
Asn	Gly	Ala	Ile	Asn	Asn	Lys	Ser	Leu	Glu	Pro	Lys	Ile	Thr	Cys	Tyr
		35				40						45			
Pro	Glu	Gly	Thr	Ser	Tyr	Ile	Phe	Leu	Asp	Asp	Val	Arg	Ile	Ser	Asn
	50					55					60				

Val	Lys	His	Asp	Gln	Glu	Asp	Ala	Gly	Val	Phe	Ile	Asn	Arg	Ser	Gly	65	70	75	80
Asn	Leu	Phe	Phe	Met	Gly	Asn	Arg	Cys	Asn	Phe	Thr	Phe	His	Asn	Leu	85	90	95	
Met	Thr	Glu	Gly	Phe	Gly	Ala	Ala	Ile	Ser	Asn	Arg	Val	Gly	Asp	Thr	100	105	110	
Thr	Leu	Thr	Leu	Ser	Asn	Phe	Ser	Tyr	Leu	Thr	Phe	Thr	Ser	Ala	Pro	115	120	125	
Leu	Leu	Pro	Gln	Gly	Gln	Gly	Ala	Ile	Tyr	Ser	Leu	Gly	Ser	Val	Met	130	135	140	
Ile	Glu	Asn	Ser	Glu	Glu	Val	Thr	Phe	Cys	Gly	Asn	Tyr	Ser	Ser	Trp	145	150	155	160
Ser	Gly	Ala	Ala	Ile	Tyr	Thr	Pro	Tyr	Leu	Leu	Gly	Ser	Lys	Ala	Ser	165	170	175	
Arg	Pro	Ser	Val	Asn	Leu	Ser	Gly	Asn	Arg	Tyr	Leu	Val	Phe	Arg	Asp	180	185	190	
Tyr	Val	Ser	Gln	Gly	Tyr	Gly	Gly	Ala	Val	Ser	Thr	His	Asn	Leu	Thr	195	200	205	
Leu	Thr	Thr	Arg	Gly	Pro	Ser	Cys	Phe	Glu	Asn	Asn	His	Ala	Tyr	His	210	215	220	
Asp	Val	Asn	Ser	Asn	Gly	Gly	Ala	Ile	Ala	Ile	Ala	Pro	Gly	Gly	Ser	225	230	235	240
Ile	Ser	Ile	Ser	Val	Lys	Ser	Gly	Asp	Leu	Ile	Phe	Lys	Gly	Asn	Thr	245	250	255	
Ala	Ser	Gln	Asp	Gly	Asn	Thr	Ile	His	Asn	Ser	Ile	His	Leu	Gln	Ser	260	265	270	
Gly	Ala	Gln	Phe	Lys	Asn	Leu	Arg	Ala	Val	Ser	Glu	Ser	Gly	Val	Tyr	275	280	285	
Phe	Tyr	Asp	Pro	Ile	Ser	His	Ser	Glu	Ser	His	Lys	Ile	Thr	Asp	Leu	290	295	300	
Val	Ile	Asn	Ala	Pro	Glu	Gly	Lys	Glu	Thr	Tyr	Glu	Gly	Thr	Ile	Ser	305	310	315	320
Phe	Ser	Gly	Leu	Cys	Leu	Asp	Asp	His	Glu	Val	Cys	Ala	Glu	Asn	Leu	325	330	335	
Thr	Ser	Thr	Ile	Leu	Gln	Asp	Val	Thr	Leu	Ala	Gly	Gly	Thr	Leu	Ser	340	345	350	
Leu	Ser	Asp	Gly	Val	Thr	Leu	Gln	Leu	His	Ser	Phe	Lys	Gln	Glu	Ala	355	360	365	

Ser Ser Thr Leu Thr Met Ser Pro Gly Thr Thr Leu Leu Cys Ser Gly
 370 375 380
 Asp Ala Arg Val Gln Asn Leu His Ile Leu Ile Glu Asp Thr Asp Asn
 385 390 395 400
 Phe Val Pro Val Arg Ile Arg Ala Glu Asp Lys Asp Ala Leu Val Ser
 405 410 415
 Leu Glu Lys Leu Lys Val Ala Phe Glu Ala Tyr Trp Ser Val Tyr Asp
 420 425 430
 Phe Pro Gln Phe Lys Glu Ala Phe Thr Ile Pro Leu Leu Glu Leu Leu
 435 440 445
 Gly Pro Ser Phe Asp Ser Leu Leu Leu Gly Glu Thr Thr Leu Glu Arg
 450 455 460
 Thr Gln Val Thr Thr Glu Asn Asp Ala Val Arg Gly Phe Trp Ser Leu
 465 470 475 480
 Ser Trp Glu Glu Tyr Pro Pro Ser Leu Asp Lys Asp Arg Arg Ile Thr
 485 490 495
 Pro Thr Lys Lys Thr Val Phe Leu Thr Trp Asn Pro Glu Ile Thr Ser
 500 505 510
 Thr Pro

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 787 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGAAAACGT	CTATTCGTAA	GTTCTTAATT	TCTACCACAC	TGGCGCCATG	TTTGCTTCA	60
ACAGCGTTTA	CTGTAGAAGT	TATCATGCCT	TCCGAGAACT	TTGATGGATC	GAGTGGGAAG	120
ATTTTTCCTT	ACACAACACT	TTCTGATCCT	AGAGGGACAC	TCTGTATTTT	TTGAGGGGAT	180
CTCTACATTG	CGAATCTTGA	TAATGCCATA	TCCAGAACCT	CTTCCAGTTG	CTTTAGCAAT	240
AGGGCGGGAG	CACTACAAAT	CTTAGGAAAA	GGTGGGGTTT	TCTCCTTCTT	AAATATCCGT	300
TCTTCAGCTG	ACGGAGCCGC	GATTAGTAGT	GTAATCACCC	AAAATCCTGA	ACTATGTCCC	360
TTGAGTTTTT	CAGGATTTAG	TCAGATGATC	TTCGATAACT	GTGAATCTTT	GACTTCAGAT	420
ACCTCAGCGA	GTAATGTCAT	ACCTCACGCA	TCGGCGATTT	ACGCTACAAC	GCCCATGCTC	480
TTTACAAACA	ATGACTCCAT	ACTATTCCAA	TACAACCGTT	CTGCAGGATT	TGGAGCTGCC	540
ATTCGAGGCA	CAAGCATCAC	AATAGAAAAT	ACGAAAAAGA	GCCTTCTCTT	TAATGGTAAT	600
GGATCCATCT	CTAATGGAGG	GGCCCTCACG	GGATCTGCAG	CGATCAACCT	CATCAACAAT	660
AGCGCTCCTG	TGATTTTCTC	AACGAATGCT	ACAGGGATCT	ATGGTGGGGC	TATTTACCTT	720
ACCGGAGGAT	CTATGCTCAC	CTCTGGGAAC	CTCTCAGGAG	TCTTGTTTCGT	TTATAATAGC	780
TCGCGCT						787

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Met Lys Thr Ser Ile Arg Lys Phe Leu Ile Ser Thr Thr Leu Ala Pro
 1             5             10             15

Cys Phe Ala Ser Thr Ala Phe Thr Val Glu Val Ile Met Pro Ser Glu
          20             25             30

Asn Phe Asp Gly Ser Ser Gly Lys Ile Phe Pro Tyr Thr Thr Leu Ser
          35             40             45

Asp Pro Arg Gly Thr Leu Cys Ile Phe Ser Gly Asp Leu Tyr Ile Ala
          50             55             60

Asn Leu Asp Asn Ala Ile Ser Arg Thr Ser Ser Ser Cys Phe Ser Asn
 65             70             75             80

Arg Ala Gly Ala Leu Gln Ile Leu Gly Lys Gly Gly Val Phe Ser Phe
          85             90             95

Leu Asn Ile Arg Ser Ser Ala Asp Gly Ala Ala Ile Ser Ser Val Ile
          100            105            110

Thr Gln Asn Pro Glu Leu Cys Pro Leu Ser Phe Ser Gly Phe Ser Gln
          115            120            125

Met Ile Phe Asp Asn Cys Glu Ser Leu Thr Ser Asp Thr Ser Ala Ser
          130            135            140

Asn Val Ile Pro His Ala Ser Ala Ile Tyr Ala Thr Thr Pro Met Leu
          145            150            155            160

Phe Thr Asn Asn Asp Ser Ile Leu Phe Gln Tyr Asn Arg Ser Ala Gly
          165            170            175

Phe Gly Ala Ala Ile Arg Gly Thr Ser Ile Thr Ile Glu Asn Thr Lys
          180            185            190

Lys Ser Leu Leu Phe Asn Gly Asn Gly Ser Ile Ser Asn Gly Gly Ala
          195            200            205

Leu Thr Gly Ser Ala Ala Ile Asn Leu Ile Asn Asn Ser Ala Pro Val
          210            215            220

Ile Phe Ser Thr Asn Ala Thr Gly Ile Tyr Gly Gly Ala Ile Tyr Leu
          225            230            235            240

Thr Gly Gly Ser Met Leu Thr Ser Gly Asn Leu Ser Gly Val Leu Phe
          245            250            255

```

Val Tyr Asn Ser Ser Arg
260

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2838 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATGAAGACTT	CAGTTTCTAT	GTTGTTGGCC	CTGCTTTGCT	CGGGGGCTAG	CTCTATTGTA	60
CTCCATGCCG	CAACCACTCC	ACTAAATCCT	GAAGATGGGT	TTATTGGGGA	GGGCAATACA	120
AATACTTTTT	CTCCGAAATC	TACAACGGAT	GCTGCAGGAA	CTACCTACTC	TCTCACAGGA	180
GAGGTTCTGT	TTATAGATCC	GGGGAAAGGT	GGTTCAATTA	CAGGAAGTTG	CTTTGTAGAA	240
ACTGCTGGCG	ATCTTACATT	TTAGGTAAT	GGAAATACCC	TAAAGTTCCT	GTCCGGTAGAT	300
GCAGGTGCTA	ATATCGCGGT	TGCTCATGTA	CAAGGAAGTA	AGAATTTAAG	CTTCACAGAT	360
TTCCTTTCTC	TGGTGATCAC	AGAATCTCCA	AAATCCGCTG	TTAGTACAGG	AAAAGGTAGC	420
CTAGTCAGTT	CAGGTGCAGT	CCAAGTGCAG	GATATAAACA	CTCTAGTTCT	TACAAGCAAT	480
GCCTCTGTCT	AAGATGGTGG	CGTGATTAAA	GGAAACTCCT	GCTTGATTCA	GGGAATCAAA	540
AATAGTGCGA	TTTTTGGACA	AAATACATCT	TCGAAAAAAG	GAGGGGCGAT	CTCCACGACT	600
CAAGGACTCA	CAATAGAGAA	TAACTTAGGG	ACGCTAAAGT	TCAATGAAAA	CAAAGCAGTG	660
ACCTCAGGAG	GCGCCTTAGA	TTTAGGAGCC	GCGTCTACAT	TCACTGCGAA	CCATGAGTTG	720
ATATTTTTCAC	AAAATAAGAC	TTCTGGGAAT	GCTGCAATG	GCGGAGCCAT	AAATTGCTCA	780
GGCGACCTAA	CATTTACTGA	TAACACTTCT	TTGTTACTTC	AAGAAAATAG	CACAATGCAG	840
GATGGTGGAG	CTTTGTGTAG	CACAGGAACC	ATAAGCATT	CCGGTAGTGA	TTCTATCAAT	900
GTGATAGGAA	ATACTTCAGG	ACAAAAAGGA	GGAGCGATTT	CTGCAGCTTC	TCTCAAGATT	960
TTGGGAGGGC	AGGGAGGCGC	TCTCTTTTCT	AATAACGTAG	TGACTCATGC	CACCCCTCTA	1020
GGAGGTGCCA	TTTTTATCAA	CACAGGAGGA	TCCTTGCAGC	TCTTCACTCA	AGGAGGGGAT	1080
ATCGTATTCG	AGGGGAATCA	GGTCACTACA	ACAGCTCCAA	ATGCTACCAC	TAAGAGAAAT	1140
GTAATTCACC	TCGAGAGCAC	CGCGAAGTGG	ACGGGACTTG	CTGCAAGTCA	AGGTAACGCT	1200
ATCTATTTCT	ATGATCCCAT	TACCACCAAC	GATACGGGAG	CAAGCGATAA	CTTACGTATC	1260
AATGAGGTCA	GTGCAATCA	AAAGCTCTCG	GGATCTATAG	TATTTTCTGG	AGAGAGATTG	1320
TCGACAGCAG	AAGCTATAGC	TGAAAATCTT	ACTTCGAGGA	TCAACCAGCC	TGTCACCTTA	1380
GTAGAGGGGA	GCTTAGAACT	TAAACAGGGA	GTGACCTTGA	TCACACAAGG	ATTCTCGCAG	1440
GAGCCAGAAT	CCACGCTTCT	TTTGGATTG	GGGACCTCAT	TACAAGCTTC	TACAGAAGAT	1500
ATCGTCATCA	CAAATTCATC	TATAAATGCC	GATACCATTT	ACGGAAAGAA	TCCAATCAAT	1560
ATTGTAGCTT	CAGCAGCGAA	TAAGAACATT	ACCCTAACAG	GAACCTTAGC	ACTTGTAAT	1620
GCAGATGGAG	CTTTGTATGA	GAACCATACC	TTGCAAGACT	CTCAAGATTA	TAGCTTTGTA	1680
AAGTTATCTC	CAGGAGCGGG	AGGGACTATA	ATTACTCAAG	ATGCTTCTCA	GAAGCTTCTT	1740
GAAGTAGCTC	CTTCTAGACC	ACATTATGGC	TATCAAGGAC	ATTGGAATGT	GCAAGTCATC	1800
CCAGGAACGG	GAAGTCAACC	GAGCCAGGCA	AATTTAGAAT	GGGTGCGGAC	AGGATACCTT	1860
CCGAATCCCG	AACGGCAAGG	ATTTTGTAGT	CCCAATAGCC	TGTGGGGTTC	TTTTGTGAT	1920
CAGCGTGCTA	TCCAAGAAAT	CATGGTAAAT	AGTAGCCAAA	TCTTATGTCA	GGAACGGGGA	1980
GTCTGGGGAG	CTGGAATTGC	TAATTTCCCTA	CATAGAGATA	AAATTAATGA	GCACGGCTAT	2040
CGCCATAGCG	GTGTCGGTTA	TCTTGTGGGA	GTTGGCACTC	ATGCTTTTTC	TGATGCTACG	2100
ATAAATGCGG	CTTTTGGCCA	GCTCTTCAGT	AGAGATAAAG	ACTACGTAGT	ATCCAAAAAT	2160
CATGGAACCT	CTACTACAGG	GGTCGTATTT	CTTGAGGATA	CCCTAGAGTT	TAGAAGTCCA	2220
CAGGGATTCT	ATACGTATAG	CTCCTCAGAA	GCTTGCTGTA	ACCAAGTCGT	CACTATAGAT	2280
ATGCAGTTGT	CTTACAGCCA	TAGAAATAAT	GATATGAAAA	CCAAATACAC	GACATATCCA	2340
GAAGCTCAGG	GATCTTGGGC	AAATGATGTT	TTTGGTCTTG	AGTTTGGAGC	GACTACATAC	2400
TACTACCCTA	ACAGTACTTT	TTTATTTGAT	TACTACTCTC	CGTTTCTCAG	GCTGCAGTGC	2460
ACCTATGCTC	ACCAGGAAGA	CTTCAAAGAG	ACAGGAGGTG	AGGTTCGTCA	CTTTACTAGC	2520

GGAGATCTTT	TCAATTTAGC	AGTTCCTATT	GGCGTGAAGT	TTGAGAGATT	TTCAGACTGT	2580
AAAAGGGGAT	CTTATGAACT	TACCCTTGCT	TATGTTCTTG	ATGTGATTCG	CAAAGATCCC	2640
AAGAGCACGG	CAACATTGGC	TAGTGGAGCT	ACGTGGAGCA	CCCACGGAAA	CAATCTCTCC	2700
AGACAAGGAT	TACAACTGCG	TTAGGGAAC	CACTGTCTCA	TAAATCCTGG	AATTGAGGTG	2760
TTCAGTCACG	GAGCTATTGA	ATTGCGGGGA	TCCTCTCGTA	ATTATAACAT	CAATCTCGGG	2820
GGTAAATACC	GATTTTAA					2838

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Lys	Thr	Ser	Val	Ser	Met	Leu	Leu	Ala	Leu	Leu	Cys	Ser	Gly	Ala	1	5	10	15
Ser	Ser	Ile	Val	Leu	His	Ala	Ala	Thr	Thr	Pro	Leu	Asn	Pro	Glu	Asp	20	25	30	
Gly	Phe	Ile	Gly	Glu	Gly	Asn	Thr	Asn	Thr	Phe	Ser	Pro	Lys	Ser	Thr	35	40	45	
Thr	Asp	Ala	Ala	Gly	Thr	Thr	Tyr	Ser	Leu	Thr	Gly	Glu	Val	Leu	Phe	50	55	60	
Ile	Asp	Pro	Gly	Lys	Gly	Gly	Ser	Ile	Thr	Gly	Thr	Cys	Phe	Val	Glu	65	70	75	80
Thr	Ala	Gly	Asp	Leu	Thr	Phe	Leu	Gly	Asn	Gly	Asn	Thr	Leu	Lys	Phe	85	90	95	
Leu	Ser	Val	Asp	Ala	Gly	Ala	Asn	Ile	Ala	Val	Ala	His	Val	Gln	Gly	100	105	110	
Ser	Lys	Asn	Leu	Ser	Phe	Thr	Asp	Phe	Leu	Ser	Leu	Val	Ile	Thr	Glu	115	120	125	
Ser	Pro	Lys	Ser	Ala	Val	Ser	Thr	Gly	Lys	Gly	Ser	Leu	Val	Ser	Ser	130	135	140	
Gly	Ala	Val	Gln	Leu	Gln	Asp	Ile	Asn	Thr	Leu	Val	Leu	Thr	Ser	Asn	145	150	155	160
Ala	Ser	Val	Glu	Asp	Gly	Gly	Val	Ile	Lys	Gly	Asn	Ser	Cys	Leu	Ile	165	170	175	
Gln	Gly	Ile	Lys	Asn	Ser	Ala	Ile	Phe	Gly	Gln	Asn	Thr	Ser	Ser	Lys	180	185	190	
Lys	Gly	Gly	Ala	Ile	Ser	Thr	Thr	Gln	Gly	Leu	Thr	Ile	Glu	Asn	Asn	195	200	205	

Leu Gly Thr Leu Lys Phe Asn Glu Asn Lys Ala Val Thr Ser Gly Gly
 210 215 220
 Ala Leu Asp Leu Gly Ala Ala Ser Thr Phe Thr Ala Asn His Glu Leu
 225 230 235 240
 Ile Phe Ser Gln Asn Lys Thr Ser Gly Asn Ala Ala Asn Gly Gly Ala
 245 250 255
 Ile Asn Cys Ser Gly Asp Leu Thr Phe Thr Asp Asn Thr Ser Leu Leu
 260 265 270
 Leu Gln Glu Asn Ser Thr Met Gln Asp Gly Gly Ala Leu Cys Ser Thr
 275 280 285
 Gly Thr Ile Ser Ile Thr Gly Ser Asp Ser Ile Asn Val Ile Gly Asn
 290 295 300
 Thr Ser Gly Gln Lys Gly Gly Ala Ile Ser Ala Ala Ser Leu Lys Ile
 305 310 315 320
 Leu Gly Gly Gln Gly Gly Ala Leu Phe Ser Asn Asn Val Val Thr His
 325 330 335
 Ala Thr Pro Leu Gly Gly Ala Ile Phe Ile Asn Thr Gly Gly Ser Leu
 340 345 350
 Gln Leu Phe Thr Gln Gly Gly Asp Ile Val Phe Glu Gly Asn Gln Val
 355 360 365
 Thr Thr Thr Ala Pro Asn Ala Thr Thr Lys Arg Asn Val Ile His Leu
 370 375 380
 Glu Ser Thr Ala Lys Trp Thr Gly Leu Ala Ala Ser Gln Gly Asn Ala
 385 390 395 400
 Ile Tyr Phe Tyr Asp Pro Ile Thr Thr Asn Asp Thr Gly Ala Ser Asp
 405 410 415
 Asn Leu Arg Ile Asn Glu Val Ser Ala Asn Gln Lys Leu Ser Gly Ser
 420 425 430
 Ile Val Phe Ser Gly Glu Arg Leu Ser Thr Ala Glu Ala Ile Ala Glu
 435 440 445
 Asn Leu Thr Ser Arg Ile Asn Gln Pro Val Thr Leu Val Glu Gly Ser
 450 455 460
 Leu Glu Leu Lys Gln Gly Val Thr Leu Ile Thr Gln Gly Phe Ser Gln
 465 470 475 480
 Glu Pro Glu Ser Thr Leu Leu Leu Asp Leu Gly Thr Ser Leu Gln Ala
 485 490 495
 Ser Thr Glu Asp Ile Val Ile Thr Asn Ser Ser Ile Asn Ala Asp Thr
 500 505 510

Ile	Tyr	Gly	Lys	Asn	Pro	Ile	Asn	Ile	Val	Ala	Ser	Ala	Ala	Asn	Lys	515	520	525	
Asn	Ile	Thr	Leu	Thr	Gly	Thr	Leu	Ala	Leu	Val	Asn	Ala	Asp	Gly	Ala	530	535	540	
Leu	Tyr	Glu	Asn	His	Thr	Leu	Gln	Asp	Ser	Gln	Asp	Tyr	Ser	Phe	Val	545	550	555	560
Lys	Leu	Ser	Pro	Gly	Ala	Gly	Gly	Thr	Ile	Ile	Thr	Gln	Asp	Ala	Ser	565	570	575	
Gln	Lys	Leu	Leu	Glu	Val	Ala	Pro	Ser	Arg	Pro	His	Tyr	Gly	Tyr	Gln	580	585	590	
Gly	His	Trp	Asn	Val	Gln	Val	Ile	Pro	Gly	Thr	Gly	Thr	Gln	Pro	Ser	595	600	605	
Gln	Ala	Asn	Leu	Glu	Trp	Val	Arg	Thr	Gly	Tyr	Leu	Pro	Asn	Pro	Glu	610	615	620	
Arg	Gln	Gly	Phe	Leu	Val	Pro	Asn	Ser	Leu	Trp	Gly	Ser	Phe	Val	Asp	625	630	635	640
Gln	Arg	Ala	Ile	Gln	Glu	Ile	Met	Val	Asn	Ser	Ser	Gln	Ile	Leu	Cys	645	650	655	
Gln	Glu	Arg	Gly	Val	Trp	Gly	Ala	Gly	Ile	Ala	Asn	Phe	Leu	His	Arg	660	665	670	
Asp	Lys	Ile	Asn	Glu	His	Gly	Tyr	Arg	His	Ser	Gly	Val	Gly	Tyr	Leu	675	680	685	
Val	Gly	Val	Gly	Thr	His	Ala	Phe	Ser	Asp	Ala	Thr	Ile	Asn	Ala	Ala	690	695	700	
Phe	Cys	Gln	Leu	Phe	Ser	Arg	Asp	Lys	Asp	Tyr	Val	Val	Ser	Lys	Asn	705	710	715	720
His	Gly	Thr	Ser	Tyr	Ser	Gly	Val	Val	Phe	Leu	Glu	Asp	Thr	Leu	Glu	725	730	735	
Phe	Arg	Ser	Pro	Gln	Gly	Phe	Tyr	Thr	Asp	Ser	Ser	Ser	Glu	Ala	Cys	740	745	750	
Cys	Asn	Gln	Val	Val	Thr	Ile	Asp	Met	Gln	Leu	Ser	Tyr	Ser	His	Arg	755	760	765	
Asn	Asn	Asp	Met	Lys	Thr	Lys	Tyr	Thr	Thr	Tyr	Pro	Glu	Ala	Gln	Gly	770	775	780	
Ser	Trp	Ala	Asn	Asp	Val	Phe	Gly	Leu	Glu	Phe	Gly	Ala	Thr	Thr	Tyr	785	790	795	800
Tyr	Tyr	Pro	Asn	Ser	Thr	Phe	Leu	Phe	Asp	Tyr	Tyr	Ser	Pro	Phe	Leu	805	810	815	

[illegible]

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3000 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 259...3000
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATCAGGTGAT	AAAAGTTCCT	CGTTAGCTAG	TGACTGTAGG	TGACATGAGA	AAGCTAACAC	60
GGAGGAAACT	AAAACCCAAG	GAATCGAAGT	CTTCATGGTA	ATGCTTTTGT	TTTTTAGAGA	120
ACTATTCGCA	TCAATATAGA	AACAAAATAA	GTAAATCAAG	TTAAAGATGA	CAAAACAGCT	180
GTCAAGAATT	TTTATCTTGA	CTCTCTGAGT	TTTCTATTTT	ATATGACGCA	AGTAAGAATT	240
TAATAATAAA	GTGGGTTT	ATG AAA TCG	CAA TTT TCC	TGG TTA GTG	CTC TCT	291
	Met Lys Ser	Gln Phe Ser	Trp Leu Val	Leu Ser		
	1	5	10			
TCG ACA TTG GCA TGT TTT ACT AGT TGT TCC ACT GTT TTT GCT GCA ACT	339					
Ser Thr Leu Ala Cys Phe Thr Ser Cys Ser Thr Val Phe Ala Ala Thr						
15 20 25						

GCT Ala	GAA Glu	AAT Asn	ATA Ile	GGC Gly	CCC Pro	TCT Ser	GAT Asp	AGC Ser	TTT Phe	GAC Asp	GGA Gly	AGT Ser	ACT Thr	AAC Asn	ACA Thr	387
	30					35					40					
GGC Gly	ACC Thr	TAT Tyr	ACT Thr	CCT Pro	AAA Lys	AAT Asn	ACG Thr	ACT Thr	ACT Thr	GGA Gly	ATA Ile	GAC Asp	TAT Tyr	ACT Thr	CTG Leu	435
	45					50					55					
ACA Thr	GGA Gly	GAT Asp	ATA Ile	ACT Thr	CTG Leu	CAA Gln	AAC Asn	CTT Leu	GGG Gly	GAT Asp	TCG Ser	GCA Ala	GCT Ala	TTA Leu	ACG Thr	483
	60				65					70					75	
AAG Lys	GGT Gly	TGT Cys	TTT Phe	TCT Ser	GAC Asp	ACT Thr	ACG Thr	GAA Glu	TCT Ser	TTA Leu	AGC Ser	TTT Phe	GCC Ala	GGT Gly	AAG Lys	531
				80				85						90		
GGG Gly	TAC Tyr	TCA Ser	CTT Leu	TCT Ser	TTT Phe	TTA Leu	AAT Asn	ATT Ile	AAG Lys	TCT Ser	AGT Ser	GCT Ala	GAA Glu	GGC Gly	GCA Ala	579
			95					100					105			
GCA Ala	CTT Leu	TCT Ser	GTT Val	ACA Thr	ACT Thr	GAT Asp	AAA Lys	AAT Asn	CTG Leu	TCG Ser	CTA Leu	ACA Thr	GGA Gly	TTT Phe	TCG Ser	627
			110				115					120				
AGT Ser	CTT Leu	ACT Thr	TTC Phe	TTA Leu	GCG Ala	GCC Ala	CCA Pro	TCA Ser	TCG Ser	GTA Val	ATC Ile	ACA Thr	ACC Thr	CCC Pro	TCA Ser	675
	125					130					135					
GGA Gly	AAA Lys	GGT Gly	GCA Ala	GTT Val	AAA Lys	TGT Cys	GGA Gly	GGG Gly	GAT Asp	CTT Leu	ACA Thr	TTT Phe	GAT Asp	AAC Asn	AAT Asn	723
	140				145					150					155	
GGA Gly	ACT Thr	ATT Ile	TTA Leu	TTT Phe	AAA Lys	CAA Gln	GAT Asp	TAC Tyr	TGT Cys	GAG Glu	GAA Glu	AAT Asn	GGC Gly	GGA Gly	GCC Ala	771
				160					165					170		
ATT Ile	TCT Ser	ACC Thr	AAG Lys	AAT Asn	CTT Leu	TCT Ser	TTG Leu	AAA Lys	AAC Asn	AGC Ser	ACG Thr	GGA Gly	TCG Ser	ATT Ile	TCT Ser	819
			175				180						185			
TTT Phe	GAA Glu	GGG Gly	AAT Asn	AAA Lys	TCG Ser	AGC Ser	GCA Ala	ACA Thr	GGG Gly	AAA Lys	AAA Lys	GGT Gly	GGG Gly	GCT Ala	ATT Ile	867
	190						195					200				
TGT Cys	GCT Ala	ACT Thr	GGT Gly	ACT Thr	GTA Val	GAT Asp	ATT Ile	ACA Thr	AAT Asn	AAT Asn	ACG Thr	GCT Ala	CCT Pro	ACC Thr	CTC Leu	915
	205					210					215					
TTC Phe	TCG Ser	AAC Asn	AAT Asn	ATT Ile	GCT Ala	GAA Glu	GCT Ala	GCA Ala	GGT Gly	GGA Gly	GCT Ala	ATA Ile	AAT Asn	AGC Ser	ACA Thr	963
	220				225					230					235	
GGA Gly	AAC Asn	TGT Cys	ACA Thr	ATT Ile	ACA Thr	GGG Gly	AAT Asn	ACG Thr	TCT Ser	CTT Leu	GTA Val	TTT Phe	TCT Ser	GAA Glu	AAT Asn	1011
				240					245					250		

AGT	GTG	ACA	GCG	ACC	GCA	GGA	AAT	GGA	GGA	GCT	CTT	TCT	GGA	GAT	GCC	1059
Ser	Val	Thr	Ala	Thr	Ala	Gly	Asn	Gly	Gly	Ala	Leu	Ser	Gly	Asp	Ala	
			255					260					265			
GAT	GTT	ACC	ATA	TCT	GGG	AAT	CAG	AGT	GTA	ACT	TTC	TCA	GGA	AAC	CAA	1107
Asp	Val	Thr	Ile	Ser	Gly	Asn	Gln	Ser	Val	Thr	Phe	Ser	Gly	Asn	Gln	
			270				275					280				
GCT	GTA	GCT	AAT	GGC	GGA	GCC	ATT	TAT	GCT	AAG	AAG	CTT	ACA	CTG	GCT	1155
Ala	Val	Ala	Asn	Gly	Gly	Ala	Ile	Tyr	Ala	Lys	Lys	Leu	Thr	Leu	Ala	
	285					290					295					
TCC	GGG	GGG	GGG	GGG	GGT	ATC	TCC	TTT	TCT	AAC	AAT	ATA	GTC	CAA	GGT	1203
Ser	Gly	Gly	Gly	Gly	Gly	Ile	Ser	Phe	Ser	Asn	Asn	Ile	Val	Gln	Gly	
300					305					310					315	
ACC	ACT	GCA	GGT	AAT	GGT	GGA	GCC	ATT	TCT	ATA	CTG	GCA	GCT	GGA	GAG	1251
Thr	Thr	Ala	Gly	Asn	Gly	Gly	Ala	Ile	Ser	Ile	Leu	Ala	Ala	Gly	Glu	
				320					325					330		
TGT	AGT	CTT	TCA	GCA	GAA	GCA	GGG	GAC	ATT	ACC	TTC	AAT	GGG	AAT	GCC	1299
Cys	Ser	Leu	Ser	Ala	Glu	Ala	Gly	Asp	Ile	Thr	Phe	Asn	Gly	Asn	Ala	
			335					340					345			
ATT	GTT	GCA	ACT	ACA	CCA	CAA	ACT	ACA	AAA	AGA	AAT	TCT	ATT	GAC	ATA	1347
Ile	Val	Ala	Thr	Thr	Pro	Gln	Thr	Thr	Lys	Arg	Asn	Ser	Ile	Asp	Ile	
			350				355					360				
GGA	TCT	ACT	GCA	AAG	ATC	ACG	AAT	TTA	CGT	GCA	ATA	TCT	GGG	CAT	AGC	1395
Gly	Ser	Thr	Ala	Lys	Ile	Thr	Asn	Leu	Arg	Ala	Ile	Ser	Gly	His	Ser	
	365					370					375					
ATC	TTT	TTC	TAC	GAT	CCG	ATT	ACT	GCT	AAT	ACG	GCT	GCG	GAT	TCT	ACA	1443
Ile	Phe	Phe	Tyr	Asp	Pro	Ile	Thr	Ala	Asn	Thr	Ala	Ala	Asp	Ser	Thr	
380					385					390					395	
GAT	ACT	TTA	AAT	CTC	AAT	AAG	GCT	GAT	GCA	GGT	AAT	AGT	ACA	GAT	TAT	1491
Asp	Thr	Leu	Asn	Leu	Asn	Lys	Ala	Asp	Ala	Gly	Asn	Ser	Thr	Asp	Tyr	
				400					405					410		
AGT	GGG	TCG	ATT	GTT	TTT	TCT	GGT	GAA	AAG	CTC	TCT	GAA	GAT	GAA	GCA	1539
Ser	Gly	Ser	Ile	Val	Phe	Ser	Gly	Glu	Lys	Leu	Ser	Glu	Asp	Glu	Ala	
			415					420					425			
AAA	GTT	GCA	GAC	AAC	CTC	ACT	TCT	ACG	CTG	AAG	CAG	CCT	GTA	ACT	CTA	1587
Lys	Val	Ala	Asp	Asn	Leu	Thr	Ser	Thr	Leu	Lys	Gln	Pro	Val	Thr	Leu	
			430				435					440				
ACT	GCA	GGA	AAT	TTA	GTA	CTT	AAA	CGT	GGT	GTC	ACT	CTC	GAT	ACG	AAA	1635
Thr	Ala	Gly	Asn	Leu	Val	Leu	Lys	Arg	Gly	Val	Thr	Leu	Asp	Thr	Lys	
	445					450					455					
GGC	TTT	ACT	CAG	ACC	GCG	GGT	TCC	TCT	GTT	ATT	ATG	GAT	GCG	GGC	ACA	1683
Gly	Phe	Thr	Gln	Thr	Ala	Gly	Ser	Ser	Val	Ile	Met	Asp	Ala	Gly	Thr	
460					465					470					475	

ACG	TTA	AAA	GCA	AGT	ACA	GAG	GAG	GTC	ACT	TTA	ACA	GGT	CTT	TCC	ATT	1731
Thr	Leu	Lys	Ala	Ser	Thr	Glu	Glu	Val	Thr	Leu	Thr	Gly	Leu	Ser	Ile	
				480					485					490		
CCT	GTA	GAC	TCT	TTA	GGC	GAG	GGT	AAG	AAA	GTT	GTA	ATT	GCT	GCT	TCT	1779
Pro	Val	Asp	Ser	Leu	Gly	Glu	Gly	Lys	Lys	Val	Val	Ile	Ala	Ala	Ser	
			495					500					505			
GCA	GCA	AGT	AAA	AAT	GTA	GCC	CTT	AGT	GGT	CCG	ATT	CTT	CTT	TTG	GAT	1827
Ala	Ala	Ser	Lys	Asn	Val	Ala	Leu	Ser	Gly	Pro	Ile	Leu	Leu	Leu	Asp	
		510					515					520				
AAC	CAA	GGG	AAT	GCT	TAT	GAA	AAT	CAC	GAC	TTA	GGA	AAA	ACT	CAA	GAC	1875
Asn	Gln	Gly	Asn	Ala	Tyr	Glu	Asn	His	Asp	Leu	Gly	Lys	Thr	Gln	Asp	
	525					530				535						
TTT	TCA	TTT	GTG	CAG	CTC	TCT	GCT	CTG	GGT	ACT	GCA	ACA	ACT	ACA	GAT	1923
Phe	Ser	Phe	Val	Gln	Leu	Ser	Ala	Leu	Gly	Thr	Ala	Thr	Thr	Thr	Asp	
540				545					550						555	
GTT	CCA	GCG	GTT	CCT	ACA	GTA	GCA	ACT	CCT	ACG	CAC	TAT	GGG	TAT	CAA	1971
Val	Pro	Ala	Val	Pro	Thr	Val	Ala	Thr	Pro	Thr	His	Tyr	Gly	Tyr	Gln	
				560					565					570		
GGT	ACT	TGG	GGA	ATG	ACT	TGG	GTT	GAT	GAT	ACC	GCA	AGC	ACT	CCA	AAG	2019
Gly	Thr	Trp	Gly	Met	Thr	Trp	Val	Asp	Asp	Thr	Ala	Ser	Thr	Pro	Lys	
			575					580					585			
ACT	AAG	ACA	GCG	ACA	TTA	GCT	TGG	ACC	AAT	ACA	GGC	TAC	CTT	CCG	AAT	2067
Thr	Lys	Thr	Ala	Thr	Leu	Ala	Trp	Thr	Asn	Thr	Gly	Tyr	Leu	Pro	Asn	
		590					595					600				
CCT	GAG	CGT	CAA	GGA	CCT	TTA	GTT	CCT	AAT	AGC	CTT	TGG	GGA	TCT	TTT	2115
Pro	Glu	Arg	Gln	Gly	Pro	Leu	Val	Pro	Asn	Ser	Leu	Trp	Gly	Ser	Phe	
	605					610					615					
TCA	GAC	ATC	CAA	GCG	ATT	CAA	GGT	GTC	ATA	GAG	AGA	AGT	GCT	TTG	ACT	2163
Ser	Asp	Ile	Gln	Ala	Ile	Gln	Gly	Val	Ile	Glu	Arg	Ser	Ala	Leu	Thr	
620					625				630						635	
CTT	TGT	TCA	GAT	CGA	GGC	TTC	TGG	GCT	GCG	GGA	GTC	GCC	AAT	TTC	TTA	2211
Leu	Cys	Ser	Asp	Arg	Gly	Phe	Trp	Ala	Ala	Gly	Val	Ala	Asn	Phe	Leu	
				640				645						650		
GAT	AAA	GAT	AAG	AAA	GGG	GAA	AAA	CGC	AAA	TAC	CGT	CAT	AAA	TCT	GGT	2259
Asp	Lys	Asp	Lys	Lys	Gly	Glu	Lys	Arg	Lys	Tyr	Arg	His	Lys	Ser	Gly	
			655					660					665			
GGA	TAT	GCT	ATC	GGA	GGT	GCA	GCG	CAA	ACT	TGT	TCT	GAA	AAC	TTA	ATT	2307
Gly	Tyr	Ala	Ile	Gly	Gly	Ala	Ala	Gln	Thr	Cys	Ser	Glu	Asn	Leu	Ile	
		670					675					680				
AGC	TTT	GCC	TTT	TGC	CAA	CTC	TTT	GGT	AGC	GAT	AAA	GAT	TTC	TTA	GTC	2355
Ser	Phe	Ala	Phe	Cys	Gln	Leu	Phe	Gly	Ser	Asp	Lys	Asp	Phe	Leu	Val	
	685					690					695					

GCT AAA AAT CAT ACT GAT ACC TAT GCA GGA GCC TTC TAT ATC CAA CAC	2403
Ala Lys Asn His Thr Asp Thr Tyr Ala Gly Ala Phe Tyr Ile Gln His	
700 705 710 715	
ATT ACA GAA TGT AGT GGG TTC ATA GGT TGT CTC TTA GAT AAA CTT CCT	2451
Ile Thr Glu Cys Ser Gly Phe Ile Gly Cys Leu Leu Asp Lys Leu Pro	
720 725 730	
GGC TCT TGG AGT CAT AAA CCC CTC GTT TTA GAA GGG CAG CTC GCT TAT	2499
Gly Ser Trp Ser His Lys Pro Leu Val Leu Glu Gly Gln Leu Ala Tyr	
735 740 745	
AGC CAC GTC AGT AAT GAT CTG AAG ACA AAG TAT ACT GCG TAT CCT GAG	2547
Ser His Val Ser Asn Asp Leu Lys Thr Lys Tyr Thr Ala Tyr Pro Glu	
750 755 760	
GTG AAA GGT TCT TGG GGG AAT AAT GCT TTT AAC ATG ATG TTG GGA GCT	2595
Val Lys Gly Ser Trp Gly Asn Asn Ala Phe Asn Met Met Leu Gly Ala	
765 770 775	
TCT TCT CAT TCT TAT CCT GAA TAC CTG CAT TGT TTT GAT ACC TAT GCT	2643
Ser Ser His Ser Tyr Pro Glu Tyr Leu His Cys Phe Asp Thr Tyr Ala	
780 785 790 795	
CCA TAC ATC AAA CTG AAT CTG ACC TAT ATA CGT CAG GAC AGC TTC TCG	2691
Pro Tyr Ile Lys Leu Asn Leu Thr Tyr Ile Arg Gln Asp Ser Phe Ser	
800 805 810	
GAG AAA GGT ACA GAA GGA AGA TCT TTT GAT GAC AGC AAC CTC TTC AAT	2739
Glu Lys Gly Thr Glu Gly Arg Ser Phe Asp Asp Ser Asn Leu Phe Asn	
815 820 825	
TTA TCT TTG CCT ATA GGG GTG AAG TTT GAG AAG TTC TCT GAT TGT AAT	2787
Leu Ser Leu Pro Ile Gly Val Lys Phe Glu Lys Phe Ser Asp Cys Asn	
830 835 840	
GAC TTT TCT TAT GAT CTG ACT TTA TCC TAT GTT CCT GAT CTT ATC CGC	2835
Asp Phe Ser Tyr Asp Leu Thr Leu Ser Tyr Val Pro Asp Leu Ile Arg	
845 850 855	
AAT GAT CCC AAA TGC ACT ACA GCA CTT GTA ATC AGC GGA GCC TCT TGG	2883
Asn Asp Pro Lys Cys Thr Thr Ala Leu Val Ile Ser Gly Ala Ser Trp	
860 865 870 875	
GAA ACT TAT GCC AAT AAC TTA GCA CGA CAG GCC TTG CAA GTG CGT GCA	2931
Glu Thr Tyr Ala Asn Asn Leu Ala Arg Gln Ala Leu Gln Val Arg Ala	
880 885 890	
GGC AGT CAC TAC GCC TTC TCT CCT ATG TTT GAA GTG CTC GGC CAG TTT	2979
Gly Ser His Tyr Ala Phe Ser Pro Met Phe Glu Val Leu Gly Gln Phe	
895 900 905	
GTC TTT GAA GTT CGT GGA TCC	3000
Val Phe Glu Val Arg Gly Ser	
910	

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 914 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

Met Lys Ser Gln Phe Ser Trp Leu Val Leu Ser Ser Thr Leu Ala Cys
 1             5             10             15

Phe Thr Ser Cys Ser Thr Val Phe Ala Ala Thr Ala Glu Asn Ile Gly
      20             25             30

Pro Ser Asp Ser Phe Asp Gly Ser Thr Asn Thr Gly Thr Tyr Thr Pro
      35             40             45

Lys Asn Thr Thr Thr Gly Ile Asp Tyr Thr Leu Thr Gly Asp Ile Thr
      50             55             60

Leu Gln Asn Leu Gly Asp Ser Ala Ala Leu Thr Lys Gly Cys Phe Ser
      65             70             75             80

Asp Thr Thr Glu Ser Leu Ser Phe Ala Gly Lys Gly Tyr Ser Leu Ser
      85             90             95

Phe Leu Asn Ile Lys Ser Ser Ala Glu Gly Ala Ala Leu Ser Val Thr
      100            105            110

Thr Asp Lys Asn Leu Ser Leu Thr Gly Phe Ser Ser Leu Thr Phe Leu
      115            120            125

Ala Ala Pro Ser Ser Val Ile Thr Thr Pro Ser Gly Lys Gly Ala Val
      130            135            140

Lys Cys Gly Gly Asp Leu Thr Phe Asp Asn Asn Gly Thr Ile Leu Phe
      145            150            155            160

Lys Gln Asp Tyr Cys Glu Glu Asn Gly Gly Ala Ile Ser Thr Lys Asn
      165            170            175

Leu Ser Leu Lys Asn Ser Thr Gly Ser Ile Ser Phe Glu Gly Asn Lys
      180            185            190

Ser Ser Ala Thr Gly Lys Lys Gly Gly Ala Ile Cys Ala Thr Gly Thr
      195            200            205

Val Asp Ile Thr Asn Asn Thr Ala Pro Thr Leu Phe Ser Asn Asn Ile
      210            215            220

Ala Glu Ala Ala Gly Gly Ala Ile Asn Ser Thr Gly Asn Cys Thr Ile
      225            230            235            240

```

Thr Gly Asn Thr Ser Leu Val Phe Ser Glu Asn Ser Val Thr Ala Thr
 245 250 255
 Ala Gly Asn Gly Gly Ala Leu Ser Gly Asp Ala Asp Val Thr Ile Ser
 260 265 270
 Gly Asn Gln Ser Val Thr Phe Ser Gly Asn Gln Ala Val Ala Asn Gly
 275 280 285
 Gly Ala Ile Tyr Ala Lys Lys Leu Thr Leu Ala Ser Gly Gly Gly Gly
 290 295 300
 Gly Ile Ser Phe Ser Asn Asn Ile Val Gln Gly Thr Thr Ala Gly Asn
 305 310 315 320
 Gly Gly Ala Ile Ser Ile Leu Ala Ala Gly Glu Cys Ser Leu Ser Ala
 325 330 335
 Glu Ala Gly Asp Ile Thr Phe Asn Gly Asn Ala Ile Val Ala Thr Thr
 340 345 350
 Pro Gln Thr Thr Lys Arg Asn Ser Ile Asp Ile Gly Ser Thr Ala Lys
 355 360 365
 Ile Thr Asn Leu Arg Ala Ile Ser Gly His Ser Ile Phe Phe Tyr Asp
 370 375 380
 Pro Ile Thr Ala Asn Thr Ala Ala Asp Ser Thr Asp Thr Leu Asn Leu
 385 390 395 400
 Asn Lys Ala Asp Ala Gly Asn Ser Thr Asp Tyr Ser Gly Ser Ile Val
 405 410 415
 Phe Ser Gly Glu Lys Leu Ser Glu Asp Glu Ala Lys Val Ala Asp Asn
 420 425 430
 Leu Thr Ser Thr Leu Lys Gln Pro Val Thr Leu Thr Ala Gly Asn Leu
 435 440 445
 Val Leu Lys Arg Gly Val Thr Leu Asp Thr Lys Gly Phe Thr Gln Thr
 450 455 460
 Ala Gly Ser Ser Val Ile Met Asp Ala Gly Thr Thr Leu Lys Ala Ser
 465 470 475 480
 Thr Glu Glu Val Thr Leu Thr Gly Leu Ser Ile Pro Val Asp Ser Leu
 485 490 495
 Gly Glu Gly Lys Lys Val Val Ile Ala Ala Ser Ala Ala Ser Lys Asn
 500 505 510
 Val Ala Leu Ser Gly Pro Ile Leu Leu Leu Asp Asn Gln Gly Asn Ala
 515 520 525
 Tyr Glu Asn His Asp Leu Gly Lys Thr Gln Asp Phe Ser Phe Val Gln
 530 535 540
 Leu Ser Ala Leu Gly Thr Ala Thr Thr Thr Asp Val Pro Ala Val Pro
 545 550 555 560

Thr	Val	Ala	Thr	Pro	Thr	His	Tyr	Gly	Tyr	Gln	Gly	Thr	Trp	Gly	Met	565	570	575
Thr	Trp	Val	Asp	Asp	Thr	Ala	Ser	Thr	Pro	Lys	Thr	Lys	Thr	Ala	Thr	580	585	590
Leu	Ala	Trp	Thr	Asn	Thr	Gly	Tyr	Leu	Pro	Asn	Pro	Glu	Arg	Gln	Gly	595	600	605
Pro	Leu	Val	Pro	Asn	Ser	Leu	Trp	Gly	Ser	Phe	Ser	Asp	Ile	Gln	Ala	610	615	620
Ile	Gln	Gly	Val	Ile	Glu	Arg	Ser	Ala	Leu	Thr	Leu	Cys	Ser	Asp	Arg	625	630	635
Gly	Phe	Trp	Ala	Ala	Gly	Val	Ala	Asn	Phe	Leu	Asp	Lys	Asp	Lys	Lys	645	650	655
Gly	Glu	Lys	Arg	Lys	Tyr	Arg	His	Lys	Ser	Gly	Gly	Tyr	Ala	Ile	Gly	660	665	670
Gly	Ala	Ala	Gln	Thr	Cys	Ser	Glu	Asn	Leu	Ile	Ser	Phe	Ala	Phe	Cys	675	680	685
Gln	Leu	Phe	Gly	Ser	Asp	Lys	Asp	Phe	Leu	Val	Ala	Lys	Asn	His	Thr	690	695	700
Asp	Thr	Tyr	Ala	Gly	Ala	Phe	Tyr	Ile	Gln	His	Ile	Thr	Glu	Cys	Ser	705	710	715
Gly	Phe	Ile	Gly	Cys	Leu	Leu	Asp	Lys	Leu	Pro	Gly	Ser	Trp	Ser	His	725	730	735
Lys	Pro	Leu	Val	Leu	Glu	Gly	Gln	Leu	Ala	Tyr	Ser	His	Val	Ser	Asn	740	745	750
Asp	Leu	Lys	Thr	Lys	Tyr	Thr	Ala	Tyr	Pro	Glu	Val	Lys	Gly	Ser	Trp	755	760	765
Gly	Asn	Asn	Ala	Phe	Asn	Met	Met	Leu	Gly	Ala	Ser	Ser	His	Ser	Tyr	770	775	780
Pro	Glu	Tyr	Leu	His	Cys	Phe	Asp	Thr	Tyr	Ala	Pro	Tyr	Ile	Lys	Leu	785	790	795
Asn	Leu	Thr	Tyr	Ile	Arg	Gln	Asp	Ser	Phe	Ser	Glu	Lys	Gly	Thr	Glu	805	810	815
Gly	Arg	Ser	Phe	Asp	Asp	Ser	Asn	Leu	Phe	Asn	Leu	Ser	Leu	Pro	Ile	820	825	830
Gly	Val	Lys	Phe	Glu	Lys	Phe	Ser	Asp	Cys	Asn	Asp	Phe	Ser	Tyr	Asp	835	840	845
Leu	Thr	Leu	Ser	Tyr	Val	Pro	Asp	Leu	Ile	Arg	Asn	Asp	Pro	Lys	Cys	850	855	860

Thr Thr Ala Leu Val Ile Ser Gly Ala Ser Trp Glu Thr Tyr Ala Asn
 865 870 875 880

Asn Leu Ala Arg Gln Ala Leu Gln Val Arg Ala Gly Ser His Tyr Ala
 885 890 895

Phe Ser Pro Met Phe Glu Val Leu Gly Gln Phe Val Phe Glu Val Arg
 900 905 910

Gly Ser

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1200
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAT CCT AAA AAT AAA GAG TAC ACA GGG ACC ATA CTC TTT TCT GGA GAA	48
Asp Pro Lys Asn Lys Glu Tyr Thr Gly Thr Ile Leu Phe Ser Gly Glu	
1 5 10 15	
AAG AGT CTA GCA AAC GAT CCT AGG GAT TTT AAA TCT ACA ATC CCT CAG	96
Lys Ser Leu Ala Asn Asp Pro Arg Asp Phe Lys Ser Thr Ile Pro Gln	
20 25 30	
AAC GTC AAC CTG TCT GCA GGA TAC TTA GTT ATT AAA GAG GGG GCC GAA	144
Asn Val Asn Leu Ser Ala Gly Tyr Leu Val Ile Lys Glu Gly Ala Glu	
35 40 45	
GTC ACA GTT TCA AAA TTC ACG CAG TCT CCA GGA TCG CAT TTA GTT TTA	192
Val Thr Val Ser Lys Phe Thr Gln Ser Pro Gly Ser His Leu Val Leu	
50 55 60	
GAT TTA GGA ACC AAA CTG ATA GCC TCT AAG GAA GAC ATT GCC ATC ACA	240
Asp Leu Gly Thr Lys Leu Ile Ala Ser Lys Glu Asp Ile Ala Ile Thr	
65 70 75 80	
GGC CTC GCG ATA GAT ATA GAT AGC TTA AGC TCA TCC TCA ACA GCA GCT	288
Gly Leu Ala Ile Asp Ile Asp Ser Leu Ser Ser Ser Ser Thr Ala Ala	
85 90 95	
GTT ATT AAA GCA AAC ACC GCA AAT AAA CAG ATA TCC GTG ACG GAC TCT	336
Val Ile Lys Ala Asn Thr Ala Asn Lys Gln Ile Ser Val Thr Asp Ser	
100 105 110	

ATA	GAA	CTT	ATC	TCG	CCT	ACT	GGC	AAT	GCC	TAT	GAA	GAT	CTC	AGA	ATG	384
Ile	Glu	Leu	Ile	Ser	Pro	Thr	Gly	Asn	Ala	Tyr	Glu	Asp	Leu	Arg	Met	
		115					120					125				
AGA	AAT	TCA	CAG	ACG	TTC	CCT	CTG	CTC	TCT	TTA	GAG	CCT	GGA	GCC	GGG	432
Arg	Asn	Ser	Gln	Thr	Phe	Pro	Leu	Leu	Ser	Leu	Glu	Pro	Gly	Ala	Gly	
		130				135					140					
GGT	AGT	GTG	ACT	GTA	ACT	GCT	GGA	GAT	TTC	CTA	CCG	GTA	AGT	CCC	CAT	480
Gly	Ser	Val	Thr	Val	Thr	Ala	Gly	Asp	Phe	Leu	Pro	Val	Ser	Pro	His	
					150					155					160	
TAT	GGT	TTT	CAA	GGC	AAT	TGG	AAA	TTA	GCT	TGG	ACA	GGA	ACT	GGA	AAC	528
Tyr	Gly	Phe	Gln	Gly	Asn	Trp	Lys	Leu	Ala	Trp	Thr	Gly	Thr	Gly	Asn	
				165					170					175		
AAA	GTT	GGA	GAA	TTC	TTC	TGG	GAT	AAA	ATA	AAT	TAT	AAG	CCT	AGA	CCT	576
Lys	Val	Gly	Glu	Phe	Phe	Trp	Asp	Lys	Ile	Asn	Tyr	Lys	Pro	Arg	Pro	
			180					185					190			
GAA	AAA	GAA	GGA	AAT	TTA	GTT	CCT	AAT	ATC	TTG	TGG	GGG	AAT	GCT	GTA	624
Glu	Lys	Glu	Gly	Asn	Leu	Val	Pro	Asn	Ile	Leu	Trp	Gly	Asn	Ala	Val	
		195					200					205				
AAT	GTC	AGA	TCC	TTA	ATG	CAG	GTT	CAA	GAG	ACC	CAT	GCA	TCG	AGC	TTA	672
Asn	Val	Arg	Ser	Leu	Met	Gln	Val	Gln	Glu	Thr	His	Ala	Ser	Ser	Leu	
		210				215					220					
CAG	ACA	GAT	CGA	GGG	CTG	TGG	ATC	GAT	GGA	ATT	GGG	AAT	TTC	TTC	CAT	720
Gln	Thr	Asp	Arg	Gly	Leu	Trp	Ile	Asp	Gly	Ile	Gly	Asn	Phe	Phe	His	
		225			230					235					240	
GTA	TCT	GCC	TCC	GAA	GAC	AAT	ATA	AGG	TAC	CGT	CAT	AAC	AGC	GGT	GGA	768
Val	Ser	Ala	Ser	Glu	Asp	Asn	Ile	Arg	Tyr	Arg	His	Asn	Ser	Gly	Gly	
				245					250					255		
TAT	GTT	CTA	TCT	GTA	AAT	AAT	GAG	ATC	ACA	CCT	AAG	CAC	TAT	ACT	TCG	816
Tyr	Val	Leu	Ser	Val	Asn	Asn	Glu	Ile	Thr	Pro	Lys	His	Tyr	Thr	Ser	
			260				265						270			
ATG	GCA	TTT	TCC	CAA	CTC	TTT	AGT	AGA	GAC	AAA	GAC	TAT	GCG	GTT	TCC	864
Met	Ala	Phe	Ser	Gln	Leu	Phe	Ser	Arg	Asp	Lys	Asp	Tyr	Ala	Val	Ser	
		275					280					285				
AAC	AAC	GAA	TAC	AGA	ATG	TAT	TTA	GGA	TCG	TAT	CTC	TAT	CAA	TAT	ACA	912
Asn	Asn	Glu	Tyr	Arg	Met	Tyr	Leu	Gly	Ser	Tyr	Leu	Tyr	Gln	Tyr	Thr	
		290				295					300					
ACC	TCC	CTA	GGG	AAT	ATT	TTC	CGT	TAT	GCT	TCG	CGT	AAC	CCT	AAT	GTA	960
Thr	Ser	Leu	Gly	Asn	Ile	Phe	Arg	Tyr	Ala	Ser	Arg	Asn	Pro	Asn	Val	
		305			310				315						320	
AAC	GTC	GGG	ATT	CTC	TCA	AGA	AGG	TTT	CTT	CAA	AAT	CCT	CTT	ATG	ATT	1008
Asn	Val	Gly	Ile	Leu	Ser	Arg	Arg	Phe	Leu	Gln	Asn	Pro	Leu	Met	Ile	
				325					330					335		

TTT CAT TTT TTG TGT GCT TAT GGT CAT GCC ACC AAT GAT ATG AAA ACA	1056
Phe His Phe Leu Cys Ala Tyr Gly His Ala Thr Asn Asp Met Lys Thr	
340 345 350	
GAC TAC GCA AAT TTC CCT ATG GTG AAA AAC AGC TGG AGA AAC AAT TGT	1104
Asp Tyr Ala Asn Phe Pro Met Val Lys Asn Ser Trp Arg Asn Asn Cys	
355 360 365	
TGG GCT ATA AAA TGC GGA GGG AGC ATG CCT CTA TTG GTA TTT GAA AAC	1152
Trp Ala Ile Lys Cys Gly Gly Ser Met Pro Leu Leu Val Phe Glu Asn	
370 375 380	
GGA AAA CTT TTC CAA GGT GCC ATC CCA TTT ATG AAA CTA CAA TTA GTT	1200
Gly Lys Leu Phe Gln Gly Ala Ile Pro Phe Met Lys Leu Gln Leu Val	
385 390 395 400	

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Asp Pro Lys Asn Lys Glu Tyr Thr Gly Thr Ile Leu Phe Ser Gly Glu	
1 5 10 15	
Lys Ser Leu Ala Asn Asp Pro Arg Asp Phe Lys Ser Thr Ile Pro Gln	
20 25 30	
Asn Val Asn Leu Ser Ala Gly Tyr Leu Val Ile Lys Glu Gly Ala Glu	
35 40 45	
Val Thr Val Ser Lys Phe Thr Gln Ser Pro Gly Ser His Leu Val Leu	
50 55 60	
Asp Leu Gly Thr Lys Leu Ile Ala Ser Lys Glu Asp Ile Ala Ile Thr	
65 70 75 80	
Gly Leu Ala Ile Asp Ile Asp Ser Leu Ser Ser Ser Ser Thr Ala Ala	
85 90 95	
Val Ile Lys Ala Asn Thr Ala Asn Lys Gln Ile Ser Val Thr Asp Ser	
100 105 110	
Ile Glu Leu Ile Ser Pro Thr Gly Asn Ala Tyr Glu Asp Leu Arg Met	
115 120 125	
Arg Asn Ser Gln Thr Phe Pro Leu Leu Ser Leu Glu Pro Gly Ala Gly	
130 135 140	

Gly	Ser	Val	Thr	Val	Thr	Ala	Gly	Asp	Phe	Leu	Pro	Val	Ser	Pro	His	145	150	155	160
Tyr	Gly	Phe	Gln	Gly	Asn	Trp	Lys	Leu	Ala	Trp	Thr	Gly	Thr	Gly	Asn	165	170	175	
Lys	Val	Gly	Glu	Phe	Phe	Trp	Asp	Lys	Ile	Asn	Tyr	Lys	Pro	Arg	Pro	180	185	190	
Glu	Lys	Glu	Gly	Asn	Leu	Val	Pro	Asn	Ile	Leu	Trp	Gly	Asn	Ala	Val	195	200	205	
Asn	Val	Arg	Ser	Leu	Met	Gln	Val	Gln	Glu	Thr	His	Ala	Ser	Ser	Leu	210	215	220	
Gln	Thr	Asp	Arg	Gly	Leu	Trp	Ile	Asp	Gly	Ile	Gly	Asn	Phe	Phe	His	225	230	235	240
Val	Ser	Ala	Ser	Glu	Asp	Asn	Ile	Arg	Tyr	Arg	His	Asn	Ser	Gly	Gly	245	250	255	
Tyr	Val	Leu	Ser	Val	Asn	Asn	Glu	Ile	Thr	Pro	Lys	His	Tyr	Thr	Ser	260	265	270	
Met	Ala	Phe	Ser	Gln	Leu	Phe	Ser	Arg	Asp	Lys	Asp	Tyr	Ala	Val	Ser	275	280	285	
Asn	Asn	Glu	Tyr	Arg	Met	Tyr	Leu	Gly	Ser	Tyr	Leu	Tyr	Gln	Tyr	Thr	290	295	300	
Thr	Ser	Leu	Gly	Asn	Ile	Phe	Arg	Tyr	Ala	Ser	Arg	Asn	Pro	Asn	Val	305	310	315	320
Asn	Val	Gly	Ile	Leu	Ser	Arg	Arg	Phe	Leu	Gln	Asn	Pro	Leu	Met	Ile	325	330	335	
Phe	His	Phe	Leu	Cys	Ala	Tyr	Gly	His	Ala	Thr	Asn	Asp	Met	Lys	Thr	340	345	350	
Asp	Tyr	Ala	Asn	Phe	Pro	Met	Val	Lys	Asn	Ser	Trp	Arg	Asn	Asn	Cys	355	360	365	
Trp	Ala	Ile	Lys	Cys	Gly	Gly	Ser	Met	Pro	Leu	Leu	Val	Phe	Glu	Asn	370	375	380	
Gly	Lys	Leu	Phe	Gln	Gly	Ala	Ile	Pro	Phe	Met	Lys	Leu	Gln	Leu	Val	385	390	395	400

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1830 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...1830
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAT CTC ACA TTA GGG AGT CGT GAC AGT TAT AAT GGT GAT ACA AGC ACC	48
Asp Leu Thr Leu Gly Ser Arg Asp Ser Tyr Asn Gly Asp Thr Ser Thr	
1 5 10 15	
ACA GAA TTT ACT CCT AAA GCG GCA ACT TCT GAT GCT AGT GGC ACG ACC	96
Thr Glu Phe Thr Pro Lys Ala Ala Thr Ser Asp Ala Ser Gly Thr Thr	
20 25 30	
TAT ATT CTC GAT GGG GAT GTC TCG ATA AGC CAA GCA GGG AAA CAA ACG	144
Tyr Ile Leu Asp Gly Asp Val Ser Ile Ser Gln Ala Gly Lys Gln Thr	
35 40 45	
AGC TTA ACC ACA AGT TGT TTT TCT AAC ACT GCA GGA AAT CTT ACC TTC	192
Ser Leu Thr Thr Ser Cys Phe Ser Asn Thr Ala Gly Asn Leu Thr Phe	
50 55 60	
TTA GGG AAC GGA TTT TCT CTT CAT TTT GAC AAT ATT ATT TCG TCT ACT	240
Leu Gly Asn Gly Phe Ser Leu His Phe Asp Asn Ile Ile Ser Ser Thr	
65 70 75 80	
GTT GCA GGT GTT GTT GTT AGC AAT ACA GCA GCT TCT GGG ATT ACG AAA	288
Val Ala Gly Val Val Val Ser Asn Thr Ala Ala Ser Gly Ile Thr Lys	
85 90 95	
TTC TCA GGA TTT TCA ACT CTT CGG ATG CTT GCA GCT CCT AGG ACC ACA	336
Phe Ser Gly Phe Ser Thr Leu Arg Met Leu Ala Ala Pro Arg Thr Thr	
100 105 110	
GGT AAA GGA GCC ATT AAA ATT ACC GAT GGT CTG GTG TTT GAG AGT ATA	384
Gly Lys Gly Ala Ile Lys Ile Thr Asp Gly Leu Val Phe Glu Ser Ile	
115 120 125	
GGG AAT CTT GAT CCG ATT ACT GTA ACA GGA TCG ACA TCT GTT GCT GAT	432
Gly Asn Leu Asp Pro Ile Thr Val Thr Gly Ser Thr Ser Val Ala Asp	
130 135 140	
GCT CTC AAT ATT AAT AGC CCT GAT ACT GGA GAT AAC AAA GAG TAT ACG	480
Ala Leu Asn Ile Asn Ser Pro Asp Thr Gly Asp Asn Lys Glu Tyr Thr	
145 150 155 160	
GGA ACC ATA GTC TTT TCT GGA GAG AAG CTC ACG GAG GCA GAA GCT AAA	528
Gly Thr Ile Val Phe Ser Gly Glu Lys Leu Thr Glu Ala Glu Ala Lys	
165 170 175	
GAT GAG AAG AAC CGC ACT TCT AAA TTA CTT CAA AAT GTT GCT TTT AAA	576
Asp Glu Lys Asn Arg Thr Ser Lys Leu Leu Gln Asn Val Ala Phe Lys	
180 185 190	

AAT	GGG	ACT	GTA	GTT	TTA	AAA	GGT	GAT	GTC	GTT	TTA	AGT	GCG	AAC	GGT	624
Asn	Gly	Thr	Val	Val	Leu	Lys	Gly	Asp	Val	Val	Leu	Ser	Ala	Asn	Gly	
		195					200					205				
TTC	TCT	CAG	GAT	GCA	AAC	TCT	AAG	TTG	ATT	ATG	GAT	TTA	GGG	ACG	TCG	672
Phe	Ser	Gln	Asp	Ala	Asn	Ser	Lys	Leu	Ile	Met	Asp	Leu	Gly	Thr	Ser	
	210					215					220					
TTG	GTT	GCA	AAC	ACC	GAA	AGT	ATC	GAG	TTA	ACG	AAT	TTG	GAA	ATT	AAT	720
Leu	Val	Ala	Asn	Thr	Glu	Ser	Ile	Glu	Leu	Thr	Asn	Leu	Glu	Ile	Asn	
225					230					235					240	
ATA	GAC	TCT	CTC	AGG	AAC	GGG	AAA	AAG	ATA	AAA	CTC	AGT	GCT	GCC	ACA	768
Ile	Asp	Ser	Leu	Arg	Asn	Gly	Lys	Lys	Ile	Lys	Leu	Ser	Ala	Ala	Thr	
				245					250					255		
GCT	CAG	AAA	GAT	ATT	CGT	ATA	GAT	CGT	CCT	GTT	GTA	CTG	GCA	ATT	AGC	816
Ala	Gln	Lys	Asp	Ile	Arg	Ile	Asp	Arg	Pro	Val	Val	Leu	Ala	Ile	Ser	
		260						265					270			
GAT	GAG	AGT	TTT	TAT	CAA	AAT	GGC	TTT	TTG	AAT	GAG	GAC	CAT	TCC	TAT	864
Asp	Glu	Ser	Phe	Tyr	Gln	Asn	Gly	Phe	Leu	Asn	Glu	Asp	His	Ser	Tyr	
	275						280					285				
GAT	GGG	ATT	CTT	GAG	TTA	GAT	GCT	GGG	AAA	GAC	ATC	GTG	ATT	TCT	GCA	912
Asp	Gly	Ile	Leu	Glu	Leu	Asp	Ala	Gly	Lys	Asp	Ile	Val	Ile	Ser	Ala	
	290					295					300					
GAT	TCT	CGC	AGT	ATA	GAT	GCT	GTA	CAA	TCT	CCG	TAT	GGC	TAT	CAG	GGA	960
Asp	Ser	Arg	Ser	Ile	Asp	Ala	Val	Gln	Ser	Pro	Tyr	Gly	Tyr	Gln	Gly	
305					310					315					320	
AAG	TGG	ACG	ATC	AAT	TGG	TCT	ACT	GAT	GAT	AAG	AAA	GCT	ACG	GTT	TCT	1008
Lys	Trp	Thr	Ile	Asn	Trp	Ser	Thr	Asp	Asp	Lys	Lys	Ala	Thr	Val	Ser	
				325					330					335		
TGG	GCG	AAG	CAG	AGT	TTT	AAT	CCC	ACT	GCT	GAG	CAG	GAG	GCT	CCG	TTA	1056
Trp	Ala	Lys	Gln	Ser	Phe	Asn	Pro	Thr	Ala	Glu	Gln	Glu	Ala	Pro	Leu	
			340					345					350			
GTT	CCT	AAT	CTT	CTT	TGG	GGT	TCT	TTT	ATA	GAT	GTT	CGT	TCC	TTC	CAG	1104
Val	Pro	Asn	Leu	Leu	Trp	Gly	Ser	Phe	Ile	Asp	Val	Arg	Ser	Phe	Gln	
		355					360					365				
AAT	TTT	ATA	GAG	CTA	GGT	ACT	GAA	GGT	GCT	CCT	TAC	GAA	AAG	AGA	TTT	1152
Asn	Phe	Ile	Glu	Leu	Gly	Thr	Glu	Gly	Ala	Pro	Tyr	Glu	Lys	Arg	Phe	
	370					375					380					
TGG	GTT	GCA	GGC	ATT	TCC	AAT	GTT	TTG	CAT	AGG	AGC	GGT	CGT	GAA	AAT	1200
Trp	Val	Ala	Gly	Ile	Ser	Asn	Val	Leu	His	Arg	Ser	Gly	Arg	Glu	Asn	
385					390					395					400	
CAA	AGG	AAA	TTC	CGT	CAT	GTG	AGT	GGA	GGT	GCT	GTA	GTA	GGT	GCT	AGC	1248
Gln	Arg	Lys	Phe	Arg	His	Val	Ser	Gly	Gly	Ala	Val	Val	Gly	Ala	Ser	
				405					410					415		

ACG AGG ATG CCG GGT GGT GAT ACC TTG TCT CTG GGT TTT GCT CAG CTC	1296
Thr Arg Met Pro Gly Gly Asp Thr Leu Ser Leu Gly Phe Ala Gln Leu	
420 425 430	
TTT GCG CGT GAC AAA GAC TAC TTT ATG AAT ACC AAT TTC GCA AAG ACC	1344
Phe Ala Arg Asp Lys Asp Tyr Phe Met Asn Thr Asn Phe Ala Lys Thr	
435 440 445	
TAC GCA GGA TCT TTA CGT TTG CAG CAC GAT GCT TCC CTA TAC TCT GTG	1392
Tyr Ala Gly Ser Leu Arg Leu Gln His Asp Ala Ser Leu Tyr Ser Val	
450 455 460	
GTG AGT ATC CTT TTA GGA GAG GGA GGA CTC CGC GAG ATC CTG TTG CCT	1440
Val Ser Ile Leu Leu Gly Glu Gly Gly Leu Arg Glu Ile Leu Leu Pro	
465 470 475 480	
TAT GTT TCC AAT ACT CTG CCG TGC TCT TTC TAT GGG CAG CTT AGC TAC	1488
Tyr Val Ser Asn Thr Leu Pro Cys Ser Phe Tyr Gly Gln Leu Ser Tyr	
485 490 495	
GGC CAT ACG GAT CAT CGC ATG AAG ACC GAG TCT CTA CCC CCC CCC CCC	1536
Gly His Thr Asp His Arg Met Lys Thr Glu Ser Leu Pro Pro Pro Pro	
500 505 510	
CCG ACG CTC TCG ACG GAT CAT ACT TCT TGG GGA GGA TAT GTC TGG GCT	1584
Pro Thr Leu Ser Thr Asp His Thr Ser Trp Gly Gly Tyr Val Trp Ala	
515 520 525	
GGA GAG CTG GGA ACT CGA GTT GCT GTT GAA AAT ACC AGC GGC AGA GGA	1632
Gly Glu Leu Gly Thr Arg Val Ala Val Glu Asn Thr Ser Gly Arg Gly	
530 535 540	
TTT TTC CGA GAG TAC ACT CCA TTT GTA AAA GTC CAA GCT GTT TAC TCG	1680
Phe Phe Arg Glu Tyr Thr Pro Phe Val Lys Val Gln Ala Val Tyr Ser	
545 550 555 560	
CGC CAA GAT AGC TTT GTT GAA CTA GGA GCT ATC AGT CGT GAT TTT AGT	1728
Arg Gln Asp Ser Phe Val Glu Leu Gly Ala Ile Ser Arg Asp Phe Ser	
565 570 575	
GAT TCG CAT CTT TAT AAC CTT GCG ATT CCT CTT GGA ATC AAG TTA GAG	1776
Asp Ser His Leu Tyr Asn Leu Ala Ile Pro Leu Gly Ile Lys Leu Glu	
580 585 590	
AAA CGG TTT GCA GAG CAA TAT TAT CAT GTT GTT GCG ATG TAT TCT CCA	1824
Lys Arg Phe Ala Glu Gln Tyr Tyr His Val Val Ala Met Tyr Ser Pro	
595 600 605	
GAT GTT	1830
Asp Val	
610	

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 610 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Asp	Leu	Thr	Leu	Gly	Ser	Arg	Asp	Ser	Tyr	Asn	Gly	Asp	Thr	Ser	Thr	1	5	10	15
Thr	Glu	Phe	Thr	Pro	Lys	Ala	Ala	Thr	Ser	Asp	Ala	Ser	Gly	Thr	Thr	20	25	30	
Tyr	Ile	Leu	Asp	Gly	Asp	Val	Ser	Ile	Ser	Gln	Ala	Gly	Lys	Gln	Thr	35	40	45	
Ser	Leu	Thr	Thr	Ser	Cys	Phe	Ser	Asn	Thr	Ala	Gly	Asn	Leu	Thr	Phe	50	55	60	
Leu	Gly	Asn	Gly	Phe	Ser	Leu	His	Phe	Asp	Asn	Ile	Ile	Ser	Ser	Thr	65	70	75	80
Val	Ala	Gly	Val	Val	Val	Ser	Asn	Thr	Ala	Ala	Ser	Gly	Ile	Thr	Lys	85	90	95	
Phe	Ser	Gly	Phe	Ser	Thr	Leu	Arg	Met	Leu	Ala	Ala	Pro	Arg	Thr	Thr	100	105	110	
Gly	Lys	Gly	Ala	Ile	Lys	Ile	Thr	Asp	Gly	Leu	Val	Phe	Glu	Ser	Ile	115	120	125	
Gly	Asn	Leu	Asp	Pro	Ile	Thr	Val	Thr	Gly	Ser	Thr	Ser	Val	Ala	Asp	130	135	140	
Ala	Leu	Asn	Ile	Asn	Ser	Pro	Asp	Thr	Gly	Asp	Asn	Lys	Glu	Tyr	Thr	145	150	155	160
Gly	Thr	Ile	Val	Phe	Ser	Gly	Glu	Lys	Leu	Thr	Glu	Ala	Glu	Ala	Lys	165	170	175	
Asp	Glu	Lys	Asn	Arg	Thr	Ser	Lys	Leu	Leu	Gln	Asn	Val	Ala	Phe	Lys	180	185	190	
Asn	Gly	Thr	Val	Val	Leu	Lys	Gly	Asp	Val	Val	Leu	Ser	Ala	Asn	Gly	195	200	205	
Phe	Ser	Gln	Asp	Ala	Asn	Ser	Lys	Leu	Ile	Met	Asp	Leu	Gly	Thr	Ser	210	215	220	
Leu	Val	Ala	Asn	Thr	Glu	Ser	Ile	Glu	Leu	Thr	Asn	Leu	Glu	Ile	Asn	225	230	235	240
Ile	Asp	Ser	Leu	Arg	Asn	Gly	Lys	Lys	Ile	Lys	Leu	Ser	Ala	Ala	Thr	245	250	255	

Ala	Gln	Lys	Asp	Ile	Arg	Ile	Asp	Arg	Pro	Val	Val	Leu	Ala	Ile	Ser		
			260					265					270				
Asp	Glu	Ser	Phe	Tyr	Gln	Asn	Gly	Phe	Leu	Asn	Glu	Asp	His	Ser	Tyr		
		275					280					285					
Asp	Gly	Ile	Leu	Glu	Leu	Asp	Ala	Gly	Lys	Asp	Ile	Val	Ile	Ser	Ala		
	290					295					300						
Asp	Ser	Arg	Ser	Ile	Asp	Ala	Val	Gln	Ser	Pro	Tyr	Gly	Tyr	Gln	Gly		
305					310					315					320		
Lys	Trp	Thr	Ile	Asn	Trp	Ser	Thr	Asp	Asp	Lys	Lys	Ala	Thr	Val	Ser		
				325					330					335			
Trp	Ala	Lys	Gln	Ser	Phe	Asn	Pro	Thr	Ala	Glu	Gln	Glu	Ala	Pro	Leu		
			340					345					350				
Val	Pro	Asn	Leu	Leu	Trp	Gly	Ser	Phe	Ile	Asp	Val	Arg	Ser	Phe	Gln		
		355					360					365					
Asn	Phe	Ile	Glu	Leu	Gly	Thr	Glu	Gly	Ala	Pro	Tyr	Glu	Lys	Arg	Phe		
	370					375					380						
Trp	Val	Ala	Gly	Ile	Ser	Asn	Val	Leu	His	Arg	Ser	Gly	Arg	Glu	Asn		
385					390					395					400		
Gln	Arg	Lys	Phe	Arg	His	Val	Ser	Gly	Gly	Ala	Val	Val	Gly	Ala	Ser		
				405					410					415			
Thr	Arg	Met	Pro	Gly	Gly	Asp	Thr	Leu	Ser	Leu	Gly	Phe	Ala	Gln	Leu		
			420					425					430				
Phe	Ala	Arg	Asp	Lys	Asp	Tyr	Phe	Met	Asn	Thr	Asn	Phe	Ala	Lys	Thr		
		435					440					445					
Tyr	Ala	Gly	Ser	Leu	Arg	Leu	Gln	His	Asp	Ala	Ser	Leu	Tyr	Ser	Val		
	450					455					460						
Val	Ser	Ile	Leu	Leu	Gly	Glu	Gly	Gly	Leu	Arg	Glu	Ile	Leu	Leu	Pro		
465					470					475					480		
Tyr	Val	Ser	Asn	Thr	Leu	Pro	Cys	Ser	Phe	Tyr	Gly	Gln	Leu	Ser	Tyr		
			485						490					495			
Gly	His	Thr	Asp	His	Arg	Met	Lys	Thr	Glu	Ser	Leu	Pro	Pro	Pro	Pro		
			500					505					510				
Pro	Thr	Leu	Ser	Thr	Asp	His	Thr	Ser	Trp	Gly	Gly	Tyr	Val	Trp	Ala		
		515					520					525					
Gly	Glu	Leu	Gly	Thr	Arg	Val	Ala	Val	Glu	Asn	Thr	Ser	Gly	Arg	Gly		
	530					535					540						
Phe	Phe	Arg	Glu	Tyr	Thr	Pro	Phe	Val	Lys	Val	Gln	Ala	Val	Tyr	Ser		
545					550					555					560		

Arg Gln Asp Ser Phe Val Glu Leu Gly Ala Ile Ser Arg Asp Phe Ser
565 570 575

Asp Ser His Leu Tyr Asn Leu Ala Ile Pro Leu Gly Ile Lys Leu Glu
580 585 590

Lys Arg Phe Ala Glu Gln Tyr Tyr His Val Val Ala Met Tyr Ser Pro
595 600 605

Asp Val
610